

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: December 24, 2005, 12:16:53 / Search time 10.133 Seconds
(without alignments)
11494.348 Million cell updates/sec

Title: US-10-782-096-1
Perfect score: 2049
Sequence: 1 atgacatcataaataa.....atgacatcataatcaatca 2049

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBml:*

1: gb_ba:*

2: gb_in:*

3: gb_env:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

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8: gb_pr:*

9: gb_ro:*

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12: gb_un:*

13: gb_vl:*

14: gb_hcg:*

15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	2049	100.0	2049	6	CQ868318	CQ868318 Sequence
2	2016	98.4	1986	6	CQ868320	CQ868320 Sequence
3	1986	96.9	1986	6	CQ868322	CQ868322 Sequence
4	256.2	12.5	3471	1	BTU04364	BTU04364 Sequence
5	256.2	12.5	3471	1	BTU04364	BTU04364 Sequence
6	236	11.5	3435	1	AB089299	AB089299 Sequence
7	236	11.5	3504	6	BD133574	BD133574 Protein h
8	236	11.5	3504	6	BD133574	BD133574 Protein h
9	235.6	11.5	2003	6	AX543928	AX543928 Sequence
10	235.6	11.5	2010	6	CS130956	CS130956 Sequence
11	235.6	11.5	2010	6	AX543938	AX543938 Sequence
12	235.6	11.5	3507	6	BTU04365	BTU04365 Sequence
13	235.6	11.5	3507	6	BTU04365	BTU04365 Sequence
14	235.6	11.5	3621	6	CS130946	CS130946 Sequence
15	235.6	11.5	3621	6	CS132867	CS132867 Sequence
16	235.6	11.5	3621	6	AX543924	AX543924 Sequence
17	235.6	11.5	4874	6	CS130962	CS130962 Sequence
18	235.6	11.5	4874	6	AX543950	AX543950 Sequence

19	234	11.4	2003	6	AX543930	AX543930 Sequence
20	234	11.4	2022	6	CS130958	CS130958 Sequence
21	234	11.4	2022	6	AX543940	AX543940 Sequence
22	234	11.4	2022	6	CS130948	CS130948 Sequence
23	234	11.4	2022	6	AX543926	AX543926 Sequence
24	234	11.4	2022	6	CS130963	CS130963 Sequence
25	234	11.4	2022	6	AX543951	AX543951 Sequence
26	232.6	11.4	2160	1	AF076953	AF076953 Sequence
27	232.6	11.4	2220	1	BACCRVYD	BACCRVYD Sequence
28	231.4	11.3	2847	1	BTU06442	BTU06442 Sequence
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45	229.4	11.2	2965	6	AR079861	AR079861 Sequence

ALIGNMENTS

RESULT 1

LOCUS CQ868318

DEFINITION Sequence 19 from Patent WO2004074462.

ACCESSION CQ868318

VERSION CQ868318.1 GI:51998364

KEYWORDS

SOURCE Bacillus thuringiensis

ORGANISM Bacillus thuringiensis

REFERENCE

AUTHORS Carozzi N., Hargies T., Koziel M.G., Duck N.B. and Carr B.

TITLE Delta-endotoxin genes and methods for their use

JOURNAL Patent: WO 2004074462-A 19 02-SEP-2004;

FEATURES

source

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2049; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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LOCUS Sequence 21 from Patent WO2004074462.
DEFINITION CQ868320
ACCESSION CQ868320.1 GI:51998366
VERSION
KEYWORDS
SOURCE Bacillus churingiensis
ORGANISM Bacillus churingiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
REFERENCE
1 Carozzi, N., Hargies, T., Koziel, M.G., Duck, N.B. and Carr, B.
AUTHORS
TITLE Delta-endotoxin genes and methods for their use
JOURNAL Patent: WO 2004074462-A 21 02-SEP-2004;
Athenix Corporation (US)
FEATURES
source Location/Qualifiers
1. 2016
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1. 2016
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2016; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1981 AGAGAACAGAAAGTAATGATCTATTTATCAATTA 2016

RESULT 3
CDS 1986 bp DNA linear PAT 13-SEP-2004
LOCUS C0868322
DEFINITION Sequence 23 from Patent WO2004074462.
ACCESSION C0868322
VERSION C0868322.1 GI:51998368
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1
AUTHORS Carozzi,N., Hargies,T., Koziel,M.G., Duck,N.B. and Carr,B.
TITLE Delta-endotoxin genes and methods for their use
JOURNAL Patent: WO 2004074462-A 23 02-SEP-2004;
Athenix Corporation (US)
FEATURES
source location/Qualifiers
1..1986
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1..1986
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ORIGIN
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Query Match 96.9%; Score 1986; DB 6; Length 1986;
Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;
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Db 61 AGCACTAATAAGAAATGCTAATAATGTTGATGATGATGATGATGATGATGATGATGATGAT 120
Qy 184 AGCAGTATTTAGCCCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 243
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Db 181 AACAGTGTAGGACTATATCTTTCGAAATTTAGGGGTCCTTTGGCAATGATCAATTTGGA 240
Qy 304 ATATATTAGTACGCTAATAGTATTTTATGCGGCAAGGCTGATGATGATGATGATGATGAT 363
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Qy 364 GTTCTTGTGGAAGAGCTTATTAAGAAAGTATAGATGATGATGATGATGATGATGATGATGAT 423
Db 301 GTTCTTGTGGAAGAGCTTATTAAGAAAGTATAGATGATGATGATGATGATGATGATGATGAT 360
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Db 421 CTAATTAACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Qy 544 AACTTTTGGAAAGAAATGACCAAAATCAAGAAAGAACTTTAAATTTATTTGTTA 603
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Db 841 GTTAAAGAGAAATTAAGTGAAGTTTATACAGATCCAGTATGAGGTTTCTGSGGATTA 900
Qy 964 GAAAGTGAAGTGAAGTATACCTTGTGATTAATCTTAATTAATCAACTTTACCTGCTATG 1023
Db 901 GAAAGTGAAGTGAAGTATACCTTGTGATTAATCTTAATTAATCAACTTTACCTGCTATG 960
Qy 1024 GAAATTAACGCAAGACGCTCTTCTTAATACCACTTGCTTAATGATTTTGTATAT 1083


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Db      961  GAAATAAACCAAGACACGCTCCCTTAAACCACTGGCTTAATCTATATTTTGTATAT
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Db      1021  ACAAGAGCTTAGATATATGTCTGATGTGAGAAATATTTGGGAGGGCATACATAGT
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Qy      1204  CCTATTCATATTTTAAATTTTGGGAACTTTCTGTTTCAGTATGAGTCACTTGCTCT
Db      1141  CCTATTCATATTTTAAATTTTGGGAACTTTCTGTTTCAGTATGAGTCACTTGCTCT
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Db      1261  GTTATTTTAAATACATCAAAATATTAATTAATGATCTGATCTTAAAGATGCTCT
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Qy      1984  AAGACTTTTCCGAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
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Qy      2044  AATTAAT 2049
Db      1981  AATTAAT 1986

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ACCESSION  U04364
VERSION     U04364.1  GI:436832
KEYWORDS   delta-endotoxin gene, partial cds.
SOURCE      Bacillus thuringiensis
            Bacillus thuringiensis
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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REFERENCE   1 (bases 1 to 3471)
            Narva, K.E. and Fu, J.
            Novel Coleopteran-Active Toxins from Bacillus thuringiensis
            Unpublished (1994)
REFERENCE   2 (bases 1 to 3471)
            Feitelson, J.S.
            Direct Submission
            Submitted (15-DEC-1993) Jerald S. Feitelson, Molecular Biology,
            Mycogen Corporation, 4980 Carroll Canyon Road, San Diego, CA 92121,
            USA

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ORIGIN

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Query Match      12.5%; Score 256.2; DB 1; Length 3471;
Best Local Similarity 50.5%; Pred. No. 1.1e-34;
Matches 838; Conservative 0; Mismatches 778; Indels 45; Gaps 7;

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 QY 253 GGGACATATCTTTCGAATTTAGGGGTCCTTTGGCAAGTCAATCATTTGGAAATATTAAT 312
 DB 229 GGTGCAATCTAGAGCTTTAGGGGTTCCATTTGCTAGTCAAGTACCTGATTTCTAAGT 288
 QY 313 AGGCTAATAGTATTTTATGGGAG-----GGCTGATCATTTTGAAGCACTTAATGTT 366
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 QY 367 CTGTGTAAGAGCTTATTAAGAAAGTATGATCAGCGTGTAAAGAAAATGCTTTAGA 426
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QY 1255 CTTCCTCGTATATATTTAGAGAAACAGGCTAATTAATTAATTAATTAATGATCAATGGA 1314
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 QY 1555 ATGATCGTAAATATGCTTTGAAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1614
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 QY 1615 TGGGGGGGAATATGCGGTTTGTCAATCCAGACCTACTGG 1655
 DB 1603 GACATGTTATATCTAGAGGGGTCCGTATGATACAGGGTCCCTGG 1643

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 DEFINITION Sequence 1 from patent US 5554534.
 ACCESSION 125971
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 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 3471)
 AUTHORS Michaelis,T.B., Narva,K.B. and Fonceirada,L.
 TITLE Bacillus thuringiensis toxins active against scarab pests
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 Query Match 12.5%; Score 256.2; DB 6; Length 3471;
 Best Local Similarity 50.5%; Pred. No. 1.1e-34;
 Matches 888; Conservative 0; Mismatches 778; Indels 45; Gaps 7;

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 ACCESSION AB089299
 VERSION AB089299.1 GI:22122187
 KEYWORDS
 SOURCE Bacillus thuringiensis serovar galleriae
 ORGANISM Bacillus thuringiensis serovar galleriae
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
 AUTHORS Amano, S., Yamashita, C., Iizuka, T., Takeuchi, K., Yamanaka, S.,
 Cerf, D. and Yamamoto, T.
 TITLE A strain of *Bacillus thuringiensis* subsp. *galleriae* containing a
 novel cry8 gene highly toxic to *Anomala cuprea* (Coleoptera:
 Scarabaeidae)
 JOURNAL Biol. Control 28, 191-196 (2003)
 REFERENCE 2 (bases 1 to 3435)
 AUTHORS Amano, S. and Yamamoto, T.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-2002) Shin-ichiro Amano, Hokkaido University,
 Graduate school of Agriculture, N9w9, Sapporo, Hokkaido 060-8589,
 Japan (E-mail: sangaku@abs.agr.hokudai.ac.jp, Tel: 81-11-706-2423,
 Fax: 81-11-706-2423)

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Query Match 11.5%; Score 236; DB 1; Length 3435;
 Best Local Similarity 55.9%; Pred. No. 3, 6e-31;
 Matches 546; Conservative 0; Mismatches 400; Indels 30; Gaps 4;

QY 13 AAAAAATGAATATGAATATGTTGATGCTTTCAGATCAACTTAATATGCTAAT 72
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 QY 73 TGTATCCAAAGTATCCATGCAAGAAAGATCCCAATGACTATGCGAAACAGAACTAT 132
 DB 67 AATTCGTATGATACCTTTAGCAAAAGATCAAGCCCATTAAGAAACATGAATCTAT 126
 QY 133 AAGAAATGCTAATATGTTGATGCTTCAATATCAAAATTTATGATATTAAGCAGTAT 192
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 QY 253 GGAATATATCTTTCGAATTTAGGGGTCCTTTGCGAAGTCAATCATTTGGAATATTAAT 312
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 QY 427 GAGCTGAAGGTTTACAGGAAATTAAGAGCTATTAACAATGACTGCAAGATGGCTA 486
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 QY 487 GTTAACAAGATGATGACA---ATCGAGGAGGAGCTAGTAAAGCAGATGCAATGTTGAT 543
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 QY 544 AACTTTTTCGAAAGATATGCAAAATTCAGAGAAAGAACTTTGAATTTATTTGTTA 603
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 DB 709 CGTACGCCCAATATCTGATTTATTTGATGATGATTAAGTAACTGCTGATTAATTA 768
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 DB 769 AAGGATACGATCTCAGATTTGGCTGAGATATCACCAATTTCCGAAGAGAAATGAATTA 828
 QY 844 ACAGATTAATGATCTGCAATTAATTTCCAAATGATGATCAGCTAGTATGATTAAGCA 903
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 QY 964 GAAAGTGAAGTATGGA 979
 DB 949 AGTGGATGATTTTGT 964

RESULT 7
 BD133574
 LOCUS
 DEFINITION
 Protein having insecticidal activity, DNA encoding the protein, and controlling agent and controlling method of noxious organisms.

ACCESSION
 BD133574
 VERSION
 BD133574.1 GI:23228519
 KEYWORDS
 JP 2002045186-A/1.
 SOURCE
 Bacillus thuringiensis
 ORGANISM
 Bacillus thuringiensis
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 1 (bases 1 to 3504)
 Asano, S., Yamana, S., and Takeuchi, K.
 Protein having insecticidal activity, DNA encoding the protein, and controlling agent and controlling method of noxious organisms
 Patent: JP 2002045186-A 1 12-FEB-2002;
 SDB BIOTECH KK
 OS Bacillus thuringiensis
 PN JP 2002045186-A/1
 PD 12-FEB-2002
 PF 03-AUG-2000 JP 2000236140
 PI SHINICHIRO ASANO, SATOSHI YAMANAKA, KATSUYOSHI TAKEUCHI PC
 C12N15/09, A01N63/00, A01N63/02, C07K14/325, C12N1/15, C12N1/19, PC
 C12N1/20,
 PC C12N1/20, C12N1/21, C12N5/10, C12N5/10/(C12N15/09, C12R1:19), PC
 (C12N1/20, C12R1:07), C12N15/00, C12N5/00, C12N5/00, (C12N15/00, PC
 C12R1:19)
 CC protein having insecticidal activity, DNA
 encoding the protein,
 CC
 CC controlling agent and controlling method of noxious organisms
 FH Key Location/Qualifiers
 FT CDS (1)..(3501).

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ORIGIN

Query Match 11.5%; Score 236; DB 6; Length 3504;
 Best Local Similarity 55.9%; Pred. No. 3, 5e-31;
 Matches 546; Conservative 0; Mismatches 400; Indels 30; Gaps 4;

QY 13 AAAAAATGAATATGAATATGTTGATGCTTTCAGATCAACTTAATATGCTAAT 72
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 QY 193 TCTAGCCCTGAAGCTGCTTAACTGATGATGATGCTTTTAAAGGATATTAACAGTGA 252
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QY 904 GTTAAACCGAATTTAGCTAGGGAATTTATATACAGATCCAGTATGAGTTTACTGGGATTA 963
DB 889 ACAACGGCCCACTTACACGGGAAGTATATACGATCATATGATTTAACAAGAAACA 948
QY 964 GAAAGTGGAGGTATGGA 979
DB 949 AGTGTGATTTTGTGA 964

RESULT 8
BD133575 3690 bp DNA linear PAT 18-SEP-2002
LOCUS BD133575
DEFINITION Protein having insecticidal activity, DNA encoding the protein, and
controlling agent and controlling method of noxious organisms.
ACCESSION BD133575.1 GI:23228520
VERSION BD133575.1
KEYWORDS JP 2002045186-A/2.
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis; Firmicutes; Bacillales; Bacillaceae; Bacillus
cereus group.
1 (bases 1 to 3690)
Aaano,S., Yamanaoka,S. and Takeuchi,K.
Protein having insecticidal activity, DNA encoding the protein, and
controlling agent and controlling method of noxious organisms
Patent: JP 2002045186-A 2 12-FEB-2002;
SDS BIOTECH KK
OS Bacillus thuringiensis
PN JP 2002045186-A/2
PD 12-FEB-2002
PF 03-AUG-2000 JP 200236140
PI SHINICHIRO ASANO,SATOSHI YAMANAKA,KATSUYOSHI TAKEUCHI PC

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C12N15/09,A01N63/00,A01N63/02,C07K14/325,C12N1/15,C12N1/19, PC
C12N1/20,
C12N1/20,C12N1/21,C12N5/10,C12N5/10/(C12N15/09,C12R1/19), PC
(C12N1/20,C12R1/07),C12N15/00,C12N5/00,C12N5/00,(C12N15/00, PC
C12R1/19)
CC Protein having insecticidal activity, DNA
encoding the protein,
and
controlling agent and controlling method of noxious organisms
FH Key Location/Qualifiers
FT source 1..3690
location/Qualifiers
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location/Qualifiers
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Query Match 11.5%; Score 236; DB 6; Length 3690;
Best Local Similarity 55.9%; Pred. No. 3,5e-31;
Matches 546; Conservative 0; Mismatches 400; Indels 30; Gaps 4;

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QY 193 TCTAGCCCTGAACTGCTTTAAGTATGACAGATGCTTTTAAACGGTATTAACAGTGA 252
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RESULT 9
AX543928 2003 bp DNA linear PAT 23-NOV-2002
LOCUS Sequence 5 from Patent WO0234774.
DEFINITION AX543928
ACCESSION AX543928 GI:25277387
VERSION AX543928.1
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1
AUTHORS Abad,A.R., Duck,N.B., Feng,X., Flanagan,R.D., Kahn,T.W. and Sims,L.E.
TITLE Genes encoding novel proteins with pesticidal activity against coleopterans
JOURNAL Patent: WO 0234774-A 5 02-MAY-2002;
E.I. DU PONT DE NEMOURS AND COMPANY (US)
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ORIGIN
Query Match 11.5%; Score 235.6; DB 6; Length 2003;
Best Local Similarity 56.5%; Pred. No. 5.1e-31;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

Qy 13 AAAAAATAAATAATGAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 72
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Qy 193 TCTAGCCCTGAAAGCTGCTTAAAGTATGATGATGATGATGATGATGATGATGATGAT 252
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RESULT 10
CS130956 2010 bp DNA linear PAT 02-AUG-2005
LOCUS Sequence 11 from Patent WO2005066349.
DEFINITION CS130956
ACCESSION CS130956
VERSION CS130956.1 GI:71793192
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1
AUTHORS Abad,A.

TITLE
JOURNAL

Genes encoding proteins with pesticidal activity
Patent: WO 200506349-A 11 21-JUL-2005;
E.I. Du pont de nemours and company (US); Pioneer Hi-Bred
International, Inc. (US)

JOURNAL

Patent: WO 2005066349-A 11 21-JUL-2005;
E.I. Du pont de nemours and company (US) ; Pioneer Hi-Bred
International, Inc. (US)

International, Inc. (US)

International, Inc. (US)

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Db	412	GATTTGAAGGATATGATATATATTAATCAATTTATCTAACTCGCTTGAAGAAATGGAA	471						
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Db	532	AGTTTATTTTACGCAATATATATGCAATCTTTTATAGTACAAATTTTGAAGACATTCCTT	591						
Qy	604	CCAGTATATGACACAGCCGGAATTTGATTTATTTTATTTAAGATGCTGATTTATTTT	663						
Db	592	ACTGTATATGCAATGCGACGCAACTTCTATTTCTGTATTTAAAGACGCGTCAATTTT	651						
Qy	664	GGAGCAGTGGCAATTAAGGTATGAAATTCGATTAATTTATATCAAGCTACAAAGGA	723						
Db	652	GGAGAAATGGGAGTGTACACAACTACTATTTATATCAATTTATGATGCTCAATGAA	711						
Qy	724	CTGATTTAGAAATATATTAAGATCATTTGTATTAACATTTCTATTAACAGGGTTTAAATCAATTT	783						
Db	712	CTTACTGCGAATATTTCTGATCTGCTGTATTAAGTGTATTAATCTGTTTATGCAAAATTTA	771						
Qy	784	AATCGCTCAATGCTCAAGATTTGGGTGAGCTTTTAAATAGTTTGTACAGATATGACATTA	843						
Db	772	AAAGGACACAGCGCTTAAACATATGGTTGACTATTAACCAATTCGTAAGAGAAATGACACTG	831						
Qy	844	AACGTTATGATTCGCCAATATTTATTTCCAACTATGATCCAGTGGATTCATAGGA	903						
Db	832	GGGGTTTATGATGTTGTGATTTATTTCCAAATTTATGACACAGCAGTACCAATGGA	891						
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RESULT 12
 BTU04365 3507 bp DNA linear BCT 27-AUG-1994
 LOCUS Bacillus thuringiensis kumamotoensis PS50C(b) CytIII
 DEFINITION delta-endotoxin gene, partial cds.
 ACCSSION U04365

VERSION	U04365.1	GI:436834
KEYWORDS	Bacillus thuringiensis	
SOURCE	Bacillus thuringiensis	
ORGANISM	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.	
REFERENCE	1 (bases 1 to 3507)	
AUTHORS	Narva, K.E. and Fu, J.	
TITLE	Novel Coleopteran-Active Toxins from Bacillus thuringiensis	
JOURNAL	Unpublished (1994)	
REFERENCE	2 (bases 1 to 3507)	
AUTHORS	Fetelison, J.S.	
TITLE	Direct Substitution	
JOURNAL	Submitted (15-DEC-1993) Jerald S. Fetelison, Molecular Biology, Mycogen Corporation, 4980 Carrol Canyon Road, San Diego, CA 92121, USA	
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	/db_xref="GI:436835"	
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ORIGIN

Query Match 11.5%; Score 235.6; DB 1; Length 3507;

Best Local Similarity 56.5%; Pred. No. 4,2e-31; Mismatches 384; Indels 27; Gaps 4;

Matches	533;	Conservative	0;	Mismatches	384;	Indels	27;	Gaps	4;
Qy	13	AAAAATAAAAATGAATATGAAATGTTGATGCTTTACGAATCAACTTAATATGCTAAT	72						
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Qy	73	TGTTATCCAAAGTATCCATGACGAAAAAGATCCCAATATGACTATGCGAAACAGAACTAT	132						
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Qy	133	AAAGATGCTTAATATATGTTGATTCGAAATACAAATTTATGTTGATATATAGACGATAT	192						
Db	127	AAAGATTTATTTAAAAATGCTCGGGA-----TGTTAGTAATACCTT	171						
Qy	193	TCAGCCCTGAAGCTGCTTAAAGTATGACGAGATGCTGTTTAAACGGGTATTAACAGTGA	252						
Db	172	GGTTCACTGAGGATTTTCTAAGCGACAGATGACGTTAAGCGCAATTTGATATAGTA	231						

QY 253 GGGACATATCTTGAATTTAGGGGTCCTTTGGCAAGCAATCAATTTGAATTAATAGT 312
DB 232 GGTAAATTAACAGGTTTAGGGGTTCAATTTGGTGGCGAATGAGATCTTATACT 291
QY 313 AGGCTAATAGTATTTATGGG-----AGGGCTGATCCATTGGAACATTAAGTT 366
DB 292 CAATTAATTAATTTCTGTGGCCCTTCAAAACAAAGATCGAATGGAAATTTTATGAA 351
QY 367 CTGTGGAGAGCTTATTAAGAAAGATATAGATCAGCGTGAAGAAATGCTCAGA 426
DB 352 CAAGTAGAAGAACTTAAATCAAAAAATGCAAGATATGCAAGAAATTAAGCCTTTCG 411
QY 427 GAGCTAGAGGTTTACAGGAATTTATGACATATATCAAACTAGACTGCAAGCTGCTA 486
DB 412 GAATTTGAGAGGCTAGGGAATTAATTAACAATTAATCTAACTGGCTTGAAGGTGAAA 471
QY 487 GTTAACAAGATGATGACAAATCGAGGGCACTAGT---AAGCAGTATGCAATTTGAT 543
DB 472 GAAATTCGAATGTTTCAGAGGCTTACGAGATGTTGAAATCGAATTTGAAATCTTGAT 531
QY 544 AACTTTTGAAGAAATATGCAAAATTCAGGAAGAAACCTTGAATTTTATTTGTA 603
DB 532 AGTTATTTAGCGAATATATGCGCATTTTTCAGGTGACAAATTTTGAAGTACCATTCCT 591
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DB 592 ACAGTATATCAATGAGCAAACTCAATTTACTTTTATTAAGGAGCGATCAATTTT 651
QY 664 GAGACAGTGGCAATTAGTGATGAAATTCGTATATTAATATCAACTACAAAGA 723
DB 652 GGAGAAAGATGGGATGTTCTACAAAGCACTATTATTAATCTATTAATCTCAAAATGAAA 711
QY 724 CTGATTAAGAAATATAAGATCAATGATTAATCAATCTATTAACCAAGGTTTAAATCAAT 783
DB 712 CTACTGCAAAATATTTCTGACACTGTGTAAAGGTATGAATGCTTTTGAACAAATTA 771
QY 784 AATGCTCAATGCTCAAGATGGGTGAGCTTTAATAGTTTGTATGATATGACATTA 843
DB 772 AAAGCTCGAGCGCTTAACATGATGATGACTATTAACAATTCGTAGAGAAATGACATTG 831
QY 844 ACAGTATTAATCTCGCAATATTAATTTCCAACTATGATCCAGTAGATATCCATTNCA 903
DB 832 ACGGTGTTAGACGTGTGTGATTAATTTTCAAACTATGATACGGTAGATCCACTGGCA 891
QY 904 GTAAAAACGAATTTAGTAGGAAGTTTATACAGATCCAGTAG 947
DB 892 ACAACAGCTCAGCTTACAAAGGAAGTATATACAGATCCACTGG 935

RESULT 13
125972 3507 bp DNA linear PAT 07-OCT-1996
LOCUS Sequence 3 from patent US 554534.
DEFINITION 125972
ACCESSION 125972.1 GI:1605842
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3507)
AUTHORS Michael, T.B., Narva, K.B. and Poncetrada, L.
TITLE Bacillus thuringiensis toxin active against scarab pests
JOURNAL Patent: US 554534-A 3 10-SEP-1996;
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 11.5%; Score 235.6; DB 6; Length 3507;
Best Local Similarity 56.5%; Pred. No. 4.2e-31;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

QY 13 AAAAAATGAATATGAATATGATGATGCTTTACGAATCAACTCTAATATGCTAAT 72
DB 10 AATATCAAAATGAATGAATTAATATGATGACACCTTCTACATC---TGTATCCAAAT 66
QY 73 TGTATTCAGAGTATCCATGCAAAAAATCCCAAAATGATATGCGAAACAGAACTAT 132
DB 67 GATTTACAGATACCTTTTGGAAATGACCAAAATCGCTACAAATATGATAT 126
QY 133 AAAGATGCTAATATATGATGATTCGAATATACAAATTTATGATATATAGCAGCTAT 192
DB 127 AAAGATTTATTAATAATGTTCTGCGGAAA-----TGTATGAAATACCT 171
QY 193 TCTAGCCTGAGACCTGTTTAAGTATGACGATGCTGTTTAAAGGATTAACAGTGA 252
DB 172 GGTTCACCTGAGGATTTCTTAAGCAGCAAGATGCAAGTTAAGCCGCAATTTATAGTA 231
QY 253 GGGACATATCTTGAATTTAGGGGTCCTTTGGCAAGTCAATCATTTGGAATTAATAGT 312
DB 232 GGTAAATTAACAGGTTTAGGGGTTCCATTTGTTGGCCGATAGGATCTTTATAGT 291
QY 313 AGGCTAATAGTATTTTATGGG-----AGGGCTGATCCATTGGAAGCACTTAAGTT 366
DB 292 CAATTAATTAATTTCTGTGGCCCTTCAAAACAAAGATCAATGGGAATTTTATGAA 351
QY 367 CTGTGGAAGGCTTATTAAGAAAGTATATGATCAGGTGTAAGAAAAATGCTTTAGA 426
DB 352 CAAGTAGAAGAACTTAAATCAAAAAATGCAAGATATGCAAGAAATTAAGCGCTTTCG 411
QY 427 GAGCTAGAGGTTTACAGGAATTTATGACATATTAACAACTAGACTGCAAGCTGCTA 486
DB 412 GAATTTGAGAGGCTAGGGAATTAATTAACAATTAATCTAACTGCTTGAAGGTGAAA 471
QY 487 GTTAACAAGATGATGACAAATCGAGGGCACTAGT---AAGCAGTATGCAATTTGAT 543
DB 472 GAAATTCGAATGATGTTCTGAGGCTTCAAAACAAAGATCAATGGGAATTTTATGAA 531
QY 544 AACTTTTGAAGAAATATGCAAAATTCAGGAAGAAACCTTGAATTTTATTTGTTA 603
DB 532 AGTTATTTAGCAATATATATGATGATCTTTTTCAGGTGACAAATTTTGAAGTACCATTCCT 591
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DB 592 ACAGTATATCAATGAGCAAACTCAATTTCTTTTATTAAGGAGCGATCAATTTT 651
QY 664 GAGACAGTGGCAATTAGTGATGAAATTCGTATATTAATATCAACTACAAAGA 723
DB 652 GGAGAAAGATGGGATGTTCTACAAAGCACTATTATTAATCACTATATGCTCAATGAAA 711
QY 724 CTGATTAAGAAATATAAGATCAATGATTAATCAATCTATTAACCAAGGTTTAAATCAATTT 783
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QY 844 ACAGTATTAATCTCGCAATATTAATTTCCAACTATGATCCAGTAGATATCCATTNCA 903
DB 832 ACGGTGTTAGACGTGTGTGATTAATTTTCAAACTATGATACGGTAGATCACTGGCA 891
QY 904 GTAAAAACGAATTTAGTAGGAAGTTTATACAGATCCAGTAG 947
DB 892 ACAACAGCTCAGCTTACAAAGGAAGTATATACAGATCCACTGG 935

RESULT 14
CS130946 3621 bp DNA linear PAT 02-AUG-2005
LOCUS Sequence 1 from Patent WO2005066349.
DEFINITION CS130946
ACCESSION CS130946
VERSION CS130946.1 GI:71793183
KEYWORDS
SOURCE Bacillus thuringiensis

ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1
AUTHORS Abad, A.
TITLE Genes encoding proteins with pesticidal activity
JOURNAL Patent: WO 2005066349-A 1 21-JUL-2005;
E.I. Du pont de nemours and company (US); Pioneer Hi-Bred International, Inc. (US)
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ORIGIN
Query Match 11.5%; Score 235.6; DB 6; Length 3621;
Best Local Similarity 56.5%; Pred. No. 4,1e-31;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

QY 13 AAAAAATGAATATGAAATGTTGATGCTTTTACGAATCAACTCTAATATGCTAAT 72
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QY 73 TGTATCCAAAGTATCCACTGCAAAAAGATCCCAATATGCTATGCGAAACAGAACTAT 132
DB 67 GATTCTTAAACGATACCTTTTGGCAATGAGCCAAACAAATGCGGTACAAATAATGATTA 126

QY 133 AAGAATGCTAATATATGTTGATTCCAATATACAAATTTATGATATTAACAGATAT 192
DB 127 AAGATATATTAATAATGTCGCGGAAATGCTAGCAAAATACCTGTCTCA----- 177

QY 193 TCTAGCCCTGAAGCTGCTTTAAGTGTACGAGATGCTGTTTAAAGGATATTAACAGTGA 252
DB 178 -----CTGAGATACCTGTTTACGCGGCAAGATGACAGCTAAGCCGCAATGTATATATGA 221

QY 253 GGAATATATCTTTGCAATTTAAGGGGTCCCTTTGGCAAGTAAATCATTTTGAATATTAAGT 312
DB 232 GGTAAATTTACTACAGGTTTAAAGGGTCCCTTTGTTGGCGGATAGAGATCTTTTACT 291

QY 313 AGGCTAATAGGATTTTATGAGGACAGGCGCTGA-----TCCATTTGAAGCACTTATGTT 366
DB 292 CAACCTATGATATTTCTGTGGCTTACGGGGAAGAGTCAATGCGAAATTTTATGGA 351

QY 367 CTTGTTGAAGAGCTTATTAAGAAAAGTATAGATCAGCGGTGAAGAAAATGCTTTAGA 426
DB 352 CAAGTAGAAGAACTATTAATCAAAAAATGAGAAATATGCAAGATTAAGGCTTTGCG 411

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DB 412 GAATTTGAAGAGATTAGTAAATATTAATCAATTTATCTTAATCTGCGTTGAAGAAATGGAA 471

QY 487 GTTAACMAAGATGATGACAAATGCGAGGCACTAGT--AACGCAATGCAATGTTGAT 543
DB 472 GAAATCCAAATGTTTCAAGAGCTTTACGAGATGTGCAAAATGCAATTTGAAATCCGTGAT 531

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QY 604 CCAGTATATGCAAGAGCCGCAATTTGCAATTAATTTATTAAGAGATGCTGATATTTT 663
DB 592 ACTGTTATGCAATGCGAGCAACTCTTCAATTTACTTTATTAAGAGACCGTCAATTTT 651

QY 664 GGAGCAGCTGGCAATTAAGTATGATGAATTCGTGATTAATTAATATATGACATTAAGGA 723
DB 652 GGAGAAAGATGGGAGATGTCACAACTACTATTAATTAATTAATATGATGCTCAATGAAA 711

QY 724 CTGATTAAGCAATTAATTAATCATTTATTAACATTTCTATTAACAGGCTTTAAATCAATT 783
DB 712 CTTACGCGAATATATCTATCATCTGTGAAGGTGTAAGAACTGTTTGAAGCAAAATTA 771

QY 784 AATCGCTCAATAGCTCAAGATTGGGAGCTTTAATATAGGTTTCGTACAGATATGACATTA 843
DB 772 AAGGCACAGCGCTTAACAAATGCGTATATACCAATTCGTTAGAAATGACACTG 831

QY 844 ACAGATTATGATCTGCAATATTAATTTCCAAACTATGATCCAGTAGATATCCATTAGCA 903
DB 832 GCGGTTTATGATGTTGTTGATCAATTAATCCAAATTAATGACACAGCAGTAACTGAA 891

QY 904 GTRAAAACGAATGATCTAGGGAAGCTTTATACAGATCCAGTATAG 947
DB 892 ACGAAAGCAACATAACAAAGGAAAGTATATACAGATCCACTGGG 935

RESULT 15
CS132867
LOCUS CS132867 3621 bp DNA linear PAT 02-AUG-2005
DEFINITION Sequence 5 from Patent WO2005063996.
ACCESSION CS132867
VERSION CS132867.1 GI:71791818
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1
AUTHORS Abad, A.
TITLE Plant activation of insect toxin
JOURNAL Patent: WO 2005063996-A 5 14-JUL-2005;
E.I. Du pont de nemours and company (US); Pioneer Hi-Bred International, Inc. (US)
FEATURES
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ORIGIN
Query Match 11.5%; Score 235.6; DB 6; Length 3621;
Best Local Similarity 56.5%; Pred. No. 4,1e-31;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

QY 13 AAAAAATGAATATGAAATGTTGATGCTTTTACGAATCAACTCTAATATGCTAAT 72
DB 10 AATATCAAAATGAATATGAAATATATGATGACACCTTCTA---CTTCGTATCCAAT 66

QY 73 TGTATCCAAAGTATCCATAGCAAAAAGATCCAAATGACTATGCGAAACAGCACTAT 132
DB 67 GATTCTAACAGATACCTTTTGGCAATGAGCAACAAATGGCTACAAATATGATTTAT 126
QY 133 AAGATGGCTAAATATGTGTGATTCAAATACAAATTTATGGTATATAGCAGTAT 192
DB 127 AAGATTATTTAAATAATGTGCGGAAATGCTAGTAAATACCTGGTCA----- 177
QY 193 TCTAGCCCTGAGCTGCTTAAAGTATGAGATGCTGTTTAAACGGTATTAACAGTGA 252
DB 178 -----CTGAAAGACTGTTAGCGGACAAAGATGCACTAAGCGCAATTGATATAGTA 231
QY 253 GGGACTATATCTTGAATTTAGGGGTCCCTTGGCAATCATTCATTTGGAATATATAGT 312
DB 232 GGTAAATTAATACAGTTTAGGGGTCCATTTGTTGGCGAATAGTATGATCTTATACT 291
QY 313 AGGCTAATAGTATTTTATGGGCAAGGCTGA-----TCCATTTGAGCACTTATGTT 366
DB 292 CAATTAATGATATTCGTGGCCCTTCAGGGGAAAGAGTCAATGGAAATTTTATGAA 351
QY 367 CTGTGTAAGAGCTTATTAAGAAAGTATAGATCAGGCTTAAGAGAAATGCTTAGA 426
DB 352 CAAGTAGAAGAACTATTAATCAAAAATGCAAGATATGCAAGAAATTAAGCGCTTTCG 411
QY 427 GAGCTAAGAGGTTTACAGGAATTAATGAGACTATATCAAACTAGACTGCAAGCATGCTA 486
DB 412 GAATTAGAAGATTAAGTAAATTAATACCAATTAATCTAATGCGCTTGAAGAAATGGAA 471
QY 487 GTTAACAAAGATATGACAAATCGAGGGCACTAGT--AAGCAGTATGCAATTTGAT 543
DB 472 GAAATATCAATGTTCAAGAGCCTTACGAGATGTGCAAAATGCAATTTGAAATCTGGAT 531
QY 544 AACTTTTCCAAAAGAAATATGCCAAATTCAGAAAGAAACCTTGAATTTATTTGTA 603
DB 532 AGTTTATTTAGCAATATATGCTTATAGAGTGACAAATTTTGAAGTACCAATTCCTT 591
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QY 664 GAGCAAGTGGCAATTAGTGATGAATTCGTATTAATTAATATATATGATCAAGAGA 723
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DB 892 ACGAAAGCAACAAATTAAGGAAATTAATACAGATCCAGTAGG 935

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Job time: 10141 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:11:08 ; Search time 1161 Seconds
(without alignments)
11762.235 Million cell updates/sec

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Perfect score: 2049
Sequence: 1 atgattcatcataaataaa.....atgattcatcataaataa 2049

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2016	98.4	2016	13	ADR89409
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5	256.2	12.5	3471	2	AAQ27167
6	256.2	12.5	3471	2	AAQ28940
7	256.2	12.5	3471	2	AAQ38653
8	256.2	12.5	3471	2	AAQ43222
9	253	12.3	3471	2	AAQ51704
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11	235.6	11.5	2003	6	ABK87236
12	235.6	11.5	2010	6	ABK87241
13	235.6	11.5	2010	12	ADL15314
14	235.6	11.5	2010	14	ABE45616
15	235.6	11.5	3507	2	AAT43221
16	235.6	11.5	3621	2	ABK87234
17	235.6	11.5	3621	6	ADL15304
18	235.6	11.5	3621	14	ABE45606
19	235.6	11.5	3621	14	ABE34684

20	235.6	11.5	4874	6	ABK87247	ABK87247 Bacillus
21	235.6	11.5	4874	12	ADL15320	Adl15320 B. thuring
22	235.6	11.5	4874	14	ABE45622	Aeb45622 B. thuring
23	234	11.4	2003	6	ABK87237	Abk87237 Bacillus
24	234	11.4	2022	6	ABK87242	Abk87242 Bacillus
25	234	11.4	2022	12	ADL15316	Adl15316 B. thuring
26	234	11.4	2022	14	ABE45618	Aeb45618 B. thuring
27	234	11.4	3633	6	ABK87235	Abk87235 Bacillus
28	234	11.4	3633	12	ADL15306	Adl15306 B. thuring
29	234	11.4	3633	14	ABE45608	Aeb45608 B. thuring
30	234	11.4	6613	6	ABK87248	Abk87248 Bacillus
31	234	11.4	6613	12	ADL15321	Adl15321 B. thuring
32	234	11.4	6613	14	ABE45623	Aeb45623 B. thuring
33	230.6	11.3	2013	6	ABK87258	Abk87258 Bacillus
34	229.4	11.2	2013	6	ABK87245	Abk87245 Bacillus
35	229.4	11.2	2160	4	AAQ04855	AAQ04855 Bacillus
36	229.4	11.2	2965	2	AAQ06636	AAQ06636 Gene enco
37	226.4	11.0	1836	13	ADV98964	Adv98964 B. thuring
38	226.4	11.0	1947	13	ADV98963	Adv98963 B. thuring
39	226.4	11.0	1968	13	ADV98962	Adv98962 B. thuring
40	226.4	11.0	1977	13	ADV98961	Adv98961 B. thuring
41	226.4	11.0	2160	13	ADV98960	Adv98960 B. thuring
42	226.4	11.0	2918	11	ADM74716	Adm74716 B. thuring
43	225.2	11.0	2022	6	ABK87239	Abk87239 Bacillus
44	225.2	11.0	2022	12	ADL15336	Adl15336 B. thuring
45	225.2	11.0	2022	12	ADL15310	Adl15310 B. thuring

ALIGNMENTS

RESULT 1
ID ADR89407 standard; CDNA; 2049 BP.
AC ADR89407;
DT 18-NOV-2004 (first entry)
XX
DE AXMT-009 coding sequence.
XX
XX ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KM lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX
OS Bacillus thuringiensis.
FH
FT Key Location/Qualifiers
FT CDS 1..2049
FT /tag= a
FT /product= "AXMT-009"
XX
XX W02004074462-A2.
XX
XX 02-SEP-2004.
XX
XX 20-FEB-2004; 2004NO-US005829.
XX
XX 20-FEB-2003; 2003US-0448632P.
XX 20-FEB-2003; 2003US-0448633P.
XX 20-FEB-2003; 2003US-0448797P.
XX 20-FEB-2003; 2003US-0448806P.
XX 20-FEB-2003; 2003US-0448810P.
XX 20-FEB-2003; 2003US-0448812P.
XX 19-FEB-2004; 2004US-00781979.
XX 19-FEB-2004; 2004US-00782020.
XX 19-FEB-2004; 2004US-00782096.
XX 19-FEB-2004; 2004US-00782141.
XX 19-FEB-2004; 2004US-00782570.
XX 19-FEB-2004; 2004US-00783417.
XX
XX (ATHE-) ATHENIX CORP.

XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
PI WPI; 2004-635574/61.
XX P-PSDB; ADR89408.
DR
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
PS Claim 1; SEQ ID NO 19; 178bp; English.

CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxin of the invention, and methods for their production, are
CC specifically for the production of organisms with pesticide resistance,
CC specifically for the production of plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX

SO Sequence 2049 BP; 688 A; 316 C; 403 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 2049; DB 13; Length 2049;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2049; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTCATATATAAATAATGAATGTAATGTTGGATGCTTACGAATCAACTCT 60
DB 1 ATGAATTCATATATAAATAATGAATGTAATGTTGGATGCTTACGAATCAACTCT 60
QY 61 AATATGCTAATTTGTTATCCAGGTATCACTAGCAAAAGATCCAAATGACTATGCGA 120
DB 61 AATATGCTAATTTGTTATCCAGGTATCACTAGCAAAAGATCCAAATGACTATGCGA 120
QY 121 AACACGAACCTATAAGAAATGGCTTAATATGTGATTCAAATACAAATTTATTTGGAT 180
DB 121 AACACGAACCTATAAGAAATGGCTTAATATGTGATTCAAATACAAATTTATTTGGAT 180
QY 181 ATAGACGATATCTAGCCCTGGAAGCTGCTTAAAGTACAGATGCTGTTTAAACGGGT 240
DB 181 ATAGACGATATCTAGCCCTGGAAGCTGCTTAAAGTACAGATGCTGTTTAAACGGGT 240
QY 241 ATTAAAGTATGGAAGCTATATCTTTGCAATTTAGGGGTCCCTTGGCAATCAATCTT 300
DB 241 ATTAAAGTATGGAAGCTATATCTTTGCAATTTAGGGGTCCCTTGGCAATCAATCTT 300
QY 301 GGAATATTAATGTAAGCTTAATATGTTTATGGCAGAGGCTGATCCATTTGAAGCACTT 360
DB 301 GGAATATTAATGTAAGCTTAATATGTTTATGGCAGAGGCTGATCCATTTGAAGCACTT 360
QY 361 ATGATATTAATGTAAGCTTAATATGTTTATGGCAGAGGCTGATCCATTTGAAGCACTT 420
DB 361 ATGATATTAATGTAAGCTTAATATGTTTATGGCAGAGGCTGATCCATTTGAAGCACTT 420
QY 421 CTTAGAGAGCTAGAGGTTTACAGGGAATTTATGAGCTATATCAAACTAGACGCAAGCA 480
DB 421 CTTAGAGAGCTAGAGGTTTACAGGGAATTTATGAGCTATATCAAACTAGACGCAAGCA 480
QY 481 TGGCTAGTTAAACAAGATGATGACATCGAGGCACTAGTAACGCGATGCAATTTGTT 540
DB 481 TGGCTAGTTAAACAAGATGATGACATCGAGGCACTAGTAACGCGATGCAATTTGTT 540
QY 541 GATTAATCTTTGAAAGAAATATGCAAAATTCAGAGAAAGAACTTTGAAATTTTATTTG 600
DB 541 GATTAATCTTTGAAAGAAATATGCAAAATTCAGAGAAAGAACTTTGAAATTTTATTTG 600

QY 601 TTACAGATATATGACAGAGCCGGAATTTTGCAATTAATTTATTAAGAGATGCTGATTA 660
DB 601 TTACAGATATATGACAGAGCCGGAATTTTGCAATTAATTTATTAAGAGATGCTGATTA 660
QY 661 TTGAGAGCAGAGGCAATTAAGTATGATGAAATTCGTGATTAATTAATTAACAGATCA 720
DB 661 TTGAGAGCAGAGGCAATTAAGTATGATGAAATTCGTGATTAATTAATTAACAGATCA 720
QY 721 GACATGATTAAGAAATATTAAGATTCATTTGATATCAATTCATTAACAGAGGTTTAAATCA 780
DB 721 GACATGATTAAGAAATATTAAGATTCATTTGATATCAATTCATTAACAGAGGTTTAAATCA 780
QY 781 TTTAATGCTCAATGCTCAAGTTGGTGAGCTTTAATATGTTTCTACAGATATGACA 840
DB 781 TTTAATGCTCAATGCTCAAGTTGGTGAGCTTTAATATGTTTCTACAGATATGACA 840
QY 841 TTAAAGTATTAAGTATGCTCAATTTTCCAACTATGATCCAGTGGTATCCATTA 900
DB 841 TTAAAGTATTAAGTATGCTCAATTTTCCAACTATGATCCAGTGGTATCCATTA 900
QY 901 GCAGTAAAAACGAAATTTGACTAGGGAAGTTTATACAGATCCAGTAGGGTTTACTGGGGTA 960
DB 901 GCAGTAAAAACGAAATTTGACTAGGGAAGTTTATACAGATCCAGTAGGGTTTACTGGGGTA 960
QY 961 TTGAAATGAGAGTATGACCTTACCTTGGTATATCTTATATATCAACTTTACTGCT 1020
DB 961 TTGAAATGAGAGTATGACCTTACCTTGGTATATCTTATATATCAACTTTACTGCT 1020
QY 1021 ATGGAATAATTAAGCAAGAGAGGCTCTTATATACAGCTTGGTATATGATTTTGTGA 1080
DB 1021 ATGGAATAATTAAGCAAGAGAGGCTCTTATATACAGCTTGGTATATGATTTTGTGA 1080
QY 1081 TATACAGAGACTTATGATATATGCTGATGAGAAATATTTGGAGGCAATACATTA 1140
DB 1081 TATACAGAGACTTATGATATATGCTGATGAGAAATATTTGGAGGCAATACATTA 1140
QY 1141 GTTGAATAATGAAATATGATGCTGAAATTAACCATTAATCTTGTAAATCTGATTT 1200
DB 1141 GTTGAATAATGAAATATGATGCTGAAATTAACCATTAATCTTGTAAATCTGATTT 1200
QY 1201 ACTGCTATTAATTTTAAATTTTGGGAACTTCTGTTTCAATATGATGATGCTGCT 1260
DB 1201 ACTGCTATTAATTTTAAATTTTGGGAACTTCTGTTTCAATATGATGATGCTGCT 1260
QY 1261 CGTATATTTTATGAGAGAAACAGAGGCTAAATTAATTAATTAAGTATGAGATCTCG 1320
DB 1261 CGTATATTTTATGAGAGAAACAGAGGCTAAATTAATTAATTAAGTATGAGATCTCG 1320
QY 1321 AGAGTATTTTATATATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1380
DB 1321 AGAGTATTTTATATATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1380
QY 1381 CCGTCTAATCTTCCATCCCAACTATATTAATTAATTAATTAATTAATTAATTAATTAATTA 1440
DB 1381 CCGTCTAATCTTCCATCCCAACTATATTAATTAATTAATTAATTAATTAATTAATTAATTA 1440
QY 1441 CCAGAGCAGAGATTTGACGATATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 1500
DB 1441 CCAGAGCAGAGATTTGACGATATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 1500
QY 1501 AGTAGTACAGGGGATTTGATGCTTTTAAAGTGGTGGGCAATACAGATATGAT 1560
DB 1501 AGTAGTACAGGGGATTTGATGCTTTTAAAGTGGTGGGCAATACAGATATGAT 1560
QY 1561 CGTAATTAATCGTCTGAACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1620
DB 1561 CGTAATTAATCGTCTGAACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1620
QY 1621 GGGATATATGAGGTTTGTCACTCCAGGACCTATGAGGGGAAATTTGGTAAAGTCAATGAT 1680
DB 1621 GGGATATATGAGGTTTGTCACTCCAGGACCTATGAGGGGAAATTTGGTAAAGTCAATGAT 1680
QY 1681 AGTTGCAATTCATTAAGTCAAGCAACAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAG 1740
DB 1681 AGTTGCAATTCATTAAGTCAAGCAACAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAG 1740


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QY 694 ATTGCGATTAATTATATCAGACTACAGAGACTGATTAGAGAAATATAAGATCATTTGTATA 753
DB 661 ATTCGATATATATATCAGACTACAGAGACTGATTAGAGAAATATAAGATCATTTGTATA 720
QY 754 ACATTTATATACAGAGGTTTAAATCAATTTAAATCGCTCAAAATCTCAAGATGGGGAGC 813
DB 721 ACATTTATATACAGAGGTTTAAATCAATTTAAATCGCTCAAAATCTCAAGATGGGGAGC 780
QY 814 TTTAATAGGTTTGTGACAGATATGACATTTACAGATTTAGATCTCCCAATATATTTTCCA 873
DB 781 TTTAATAGGTTTGTGACAGATATGACATTTACAGATTTAGATCTCCCAATATATTTTCCA 840
QY 874 AACTATGATCCAGTAGAGTTTACTGGGGTTTAAAGAAAGTAGAGTAGATTAACCTTGTGTAT 933
DB 841 AACTATGATCCAGTAGAGTTTACTGGGGTTTAAAGAAAGTAGAGTAGATTAACCTTGTGTAT 900
QY 934 ACAGATCCAGTAGAGGTTTACTGGGGTTTAAAGAAAGTAGAGTAGATTAACCTTGTGTAT 993
DB 901 ACAGATCCAGTAGAGGTTTACTGGGGTTTAAAGAAAGTAGAGTAGATTAACCTTGTGTAT 960
QY 994 AATCTTAATATATCAACCTTTACTGCTATGAGAAATATACAGACGACGCTCTCTTAT 1053
DB 961 AATCTTAATATATCAACCTTTACTGCTATGAGAAATATACAGACGACGCTCTCTTAT 1020
QY 1054 ACCACTTGGCTTAATGCTATTTTGTATATACAGAGACTCTAGATAATATGCTGATGTG 1113
DB 1021 ACCACTTGGCTTAATGCTATTTTGTATATACAGAGACTCTAGATAATATGCTGATGTG 1080
QY 1114 AGAAATATTTGGGAGAGGCTATACATTAGTTGAAAATGAAAATAGTGTCTGAAAATAC 1173
DB 1081 AGAAATATTTGGGAGAGGCTATACATTAGTTGAAAATGAAAATAGTGTCTGAAAATAC 1140
QY 1174 CATTACTTTGGTAAACTGATTTCTATTTACTCTATTCATTAATTTTAAATTTTGGGAACTT 1233
DB 1141 CATTACTTTGGTAAACTGATTTCTATTTACTCTATTCATTAATTTTAAATTTTGGGAACTT 1200
QY 1234 TCTGTTTTCAGTATGATGCTGCTGCTATATATTTAGAGGAA CAGAGGCTAATAT 1293
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QY 1294 TATATTTACTAGTATGATGAGAGTCTGAGAGTTATTTTAAATCATCAATATATATATAT 1353
DB 1261 TATATTTACTAGTATGATGAGAGTCTGAGAGTTATTTTAAATCATCAATATATATATAT 1320
QY 1354 GTACCTGATCTTTAAGATGAGAGTGCCTGCTAATCTTCATCCCAACTATATATATCA 1413
DB 1321 GTACCTGATCTTTAAGATGAGAGTGCCTGCTAATCTTCATCCCAACTATATATATCA 1380
QY 1414 GAATTTACAGAAAGATTAAGCCAAAGCCAAAGCAGAGATTTTCAAGCATATATATCT 1473
DB 1381 GAATTTACAGAAAGATTAAGCCAAAGCCAAAGCAGAGATTTTCAAGCATATATATCT 1440
QY 1474 TATATTTCAAAATTTTATGATGACGCGCAAGTAGTTCCAGCGGTATTTGTAGTCTTTTAAAG 1533
DB 1441 TATATTTCAAAATTTTATGATGACGCGCAAGTAGTTCCAGCGGTATTTGTAGTCTTTTAAAG 1500
QY 1534 TTTGTTGGGACATACAGATATGATCGTAATATCGTTTGAACCAATATATATATCT 1593
DB 1501 TTTGTTGGGACATACAGATATGATCGTAATATCGTTTGAACCAATATATATATCT 1560
QY 1594 CAAATGATGCAATTAAGGTTTGGGGGGGGAATATCGGTTTGTCAATCCAGGACCTTACT 1653
DB 1561 CAAATGATGCAATTAAGGTTTGGGGGGGGAATATCGGTTTGTCAATCCAGGACCTTACT 1620
QY 1654 GGGGGGAATTTGGTAAAGTCAAGTATAGTTGGCATTTCACTTAAAGTTCAAGACACAA 1713
DB 1621 GGGGGGAATTTGGTAAAGTCAAGTATAGTTGGCATTTCACTTAAAGTTCAAGACACAA 1680
QY 1714 AGACAAACAAGTATATGATGTTGCTTGGCTTATGCTTGTATTAATCCCATGGGGAGTCT 1773
DB 1681 AGACAAACAAGTATATGATGTTGCTTGGCTTATGCTTGTATTAATCCCATGGGGAGTCT 1740

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QY 1774 ATTTTGTAGAACACAGCGCGAGTACTCATATAGTTTCAATTTTGTATGCTCAATTTCA 1833
DB 1741 ATTTTGTAGAACACAGCGCGAGTACTCATATAGTTTCAATTTTGTATGCTCAATTTCA 1800
QY 1834 TCAGGTCGTCCATCAACAACCTCTCTAGAGAGTATTTTGGCTATATGATGTTCCAGGT 1893
DB 1801 TCAGGTCGTCCATCAACAACCTCTCTAGAGAGTATTTTGGCTATATGATGTTCCAGGT 1860
QY 1894 ATTTTACACATCAATTAATCCCTTAATAGATATAGAACAAAGCTTGGTACCCAC 1953
DB 1861 ATTTTACACATCAATTAATCCCTTAATAGATATAGAACAAAGCTTGGTACCCAC 1920
QY 1954 GCGATAGACAAATTTGAATTTATTCACCTTAACCTTTCCGAATCAATTAAGAAAA 2013
DB 1921 GCGATAGACAAATTTGAATTTATTCACCTTAACCTTTCCGAATCAATTAAGAAAA 1980
QY 2014 AGGAAACAGAGTAATGATCTAATTTATCAATTA 2049
DB 1981 AGGAAACAGAGTAATGATCTAATTTATCAATTA 2016

RESULT 3
ADR89411
ID ADR89411 standard; cDNA; 1986 BP.
XX
AC ADR89411;
XX
DT 18-NOV-2004 (first entry)
XX
DE AKMI-009 alternative start site coding sequence #2.
XX
KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT CDS 1..1986
FT /tag= a
FT /product= "Alternative AKMI-009 #2"
XX
PN WO200407462-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
XX
PR 20-FEB-2003; 2003US-0448633P.
XX
PR 20-FEB-2003; 2003US-0448797P.
XX
PR 20-FEB-2003; 2003US-0448806P.
XX
PR 20-FEB-2003; 2003US-0448810P.
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PR 20-FEB-2003; 2003US-0448812P.
XX
PR 19-FEB-2004; 2004US-00781979.
XX
PR 19-FEB-2004; 2004US-00782020.
XX
PR 19-FEB-2004; 2004US-00782026.
XX
PR 19-FEB-2004; 2004US-00782141.
XX
PR 19-FEB-2004; 2004US-00782570.
XX
PR 19-FEB-2004; 2004US-00783417.
XX
PA (ATHE-) ATHENIX CORP.
PI
PI Carozzi N, Hargis T, Koziel MG, Duck NB, Carr B;
XX
XX WPI; 2004-635574/61.
XX
XX P-PSDB; ADR89412.
XX
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
XX and polypeptides, useful for killing lepidopteran or coleopteran pests or
XX for producing organisms with pesticide resistance.
XX

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PS Claim 1, SEQ ID NO 23, 178bp, English.

XX This sequence encodes an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. CC The nucleic acid sequences of the invention are useful in DNA constructs CC or expression cassettes for transformation and expression in plants and CC bacteria. The nucleic acids and corresponding polypeptides are useful for CC killing lepidopteran or coleopteran pests. Compositions containing the CC delta-endotoxins of the invention, and methods for their production, are CC useful for the production of organisms with pesticide resistance, CC specifically bacteria and plants. These organisms are useful for CC generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the CC presence of delta-endotoxin or delta-endotoxin-associated proteins or CC nucleic acids in products or organisms.

XX Sequence 1986 BP, 659 A, 310 C, 395 G, 622 T, 0 U, 0 Other;

Query Match 96.9%; Score 1986; DB 13; Length 1986;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1986; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 64 ATGCTTAATGTTATCCAAAGTATCCACTAGCAAAAGATCCCAAAATGACTATGCGAAAC 123
DB 1 ATGCTTAATGTTATCCAAAGTATCCACTAGCAAAAGATCCCAAAATGACTATGCGAAAC 60
QY 124 ACCAATATAAGATGGCTTAATATGATGATCAATACAAATTTATTTGATATATA 183
DB 61 ACCAATATAAGATGGCTTAATATGATGATCAATACAAATTTATTTGATATATA 120
QY 184 AGCAGCTATTCTAGCCCTGGAAGCTGTTTAAGTGTACAGATGCTGTTTAAACGGTATT 243
DB 121 AGCAGCTATTCTAGCCCTGGAAGCTGTTTAAGTGTACAGATGCTGTTTAAACGGTATT 180
QY 244 AACAGTGTAGGACTATATCTTTGCAATTTAAGGGTCCCTTTGGCAAGTCAATCTTTGA 303
DB 181 AACAGTGTAGGACTATATCTTTGCAATTTAAGGGTCCCTTTGGCAAGTCAATCTTTGA 240
QY 304 ATAATTAAGTGGCTTAATAGGATTTTATGGGCAAGGGCTGATCATTTGGAAGCATTAAG 363
DB 241 ATAATTAAGTGGCTTAATAGGATTTTATGGGCAAGGGCTGATCATTTGGAAGCATTAAG 300
QY 364 GTTCTTGTTGAAGCTTATTAAGAAAGTATAGATCAGCGTGTAAAGAAAATGCTCTT 423
DB 301 GTTCTTGTTGAAGCTTATTAAGAAAGTATAGATCAGCGTGTAAAGAAAATGCTCTT 360
QY 424 AGAAGCTAGAAAGTTTACAGGGAATTAAGACTATATCAAACTAGACTGCAAGCATGG 483
DB 361 AGAAGCTAGAAAGTTTACAGGGAATTAAGACTATATCAAACTAGACTGCAAGCATGG 420
QY 484 CTAGTTTAACAAAGATGATGACAAATCGGAGGCACTATTAACGAGTATGCAATTTGAT 543
DB 421 CTAGTTTAACAAAGATGATGACAAATCGGAGGCACTATTAACGAGTATGCAATTTGAT 480
QY 544 AACTTTTTCGAAAAGATATGCGAAATTCAGAGAAAGAACTTGAATTTTATTTATTTGTA 603
DB 481 AACTTTTTCGAAAAGATATGCGAAATTCAGAGAAAGAACTTGAATTTTATTTATTTGTA 540
QY 604 CCAATATATGACAAAGCCGGAATTTGCAATTTTATTTAAGAGATGCTGATTTATTT 663
DB 541 CCAATATATGACAAAGCCGGAATTTGCAATTTTATTTAAGAGATGCTGATTTATTT 600
QY 664 GGAAGCAAGTGGCAATTAAGTATGATGAAGAAATTCGTGATATTAATATACATACAGGA 723
DB 601 GGAAGCAAGTGGCAATTAAGTATGATGAAGAAATTCGTGATATTAATATACATACAGGA 660
QY 724 CTGATTAAGAAATTAAGATCATTTATTAACATTTCTATACACAGGTTTAAATCAATTT 783
DB 661 CTGATTAAGAAATTAAGATCATTTATTAACATTTCTATACACAGGTTTAAATCAATTT 720
QY 784 AATGCTCAAAATGCTCAAGATGGGCTGATTTAATAGTTTCGTACAGATATGACATTA 843
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DB 721 AATGCTCAAAATGCTCAAGATGGGCTGATTTAATAGTTTCGTACAGATATGACATTA 780
QY 844 ACAATATTAGATCTCGAATATTTATTTCCAAACTATGATCCAGTAGATATCCATTAGCA 903
DB 781 ACAATATTAGATCTCGAATATTTATTTCCAAACTATGATCCAGTAGATATCCATTAGCA 840
QY 904 GTAAAAACGAAATTTAGTAGGAAAGTTTATACAGATCCAGTAGGTTTACTGGGGTATTA 963
DB 841 GTAAAAACGAAATTTAGTAGGAAAGTTTATACAGATCCAGTAGGTTTACTGGGGTATTA 900
QY 964 GAAAGTGAAGTGAAGTATCCCTTGATATATCCCTTAATATCAACCTTACGCTATG 1023
DB 901 GAAAGTGAAGTGAAGTATCCCTTGATATATCCCTTAATATCAACCTTACGCTATG 960
QY 1024 GAAATATACCAAGACAGACCTCTTCTTATACACTTGCGCTATCGTATTTTGTATAT 1083
DB 961 GAAATATACCAAGACAGACCTCTTCTTATACACTTGCGCTATCGTATTTTGTATAT 1020
QY 1084 ACAAGACTCTAGATATATGCTGATGAGAAATTTTGGAGGCAATACATTAGTT 1143
DB 1021 ACAAGACTCTAGATATATGCTGATGAGAAATTTTGGAGGCAATACATTAGTT 1080
QY 1144 GAAATATGAATATGATGTTGTAATTAACCATTAATCTGTAAACCTGATTTCTATAC 1203
DB 1081 GAAATATGAATATGATGTTGTAATTAACCATTAATCTGTAAACCTGATTTCTATAC 1140
QY 1204 CCTATTCAATATTTTATTTTGGCAACCTTCTGTTCAGTATGAGTCACTTGCCT 1263
DB 1141 CCTATTCAATATTTTATTTTGGCAACCTTCTGTTCAGTATGAGTCACTTGCCT 1200
QY 1264 ATATATTTAGAGAAACAGAGGCTAATATTAATTAATTAATGATAGATGAGTCTCGAGA 1323
DB 1201 ATATATTTAGAGAAACAGAGGCTAATATTAATTAATTAATGATAGATGAGTCTCGAGA 1260
QY 1324 GTTATTTTATATCATCAAAATTAATTAATGATACCTGATCTTTAAGATACGAAGTCC 1383
DB 1261 GTTATTTTATATCATCAAAATTAATTAATGATACCTGATCTTTAAGATACGAAGTCC 1320
QY 1384 GCTAATCTTCATCCCAACTATATATATGAGATTAACAGAAAGATAAGCAAGCA 1443
DB 1321 GCTAATCTTCATCCCAACTATATATATGAGATTAACAGAAAGATAAGCAAGCA 1380
QY 1444 AACGAGAGATTTACGCCATAGATTAATCTTATATATCAAAATTTGATGACGCGGAAGT 1503
DB 1381 AACGAGAGATTTACGCCATAGATTAATCTTATATATCAAAATTTGATGACGCGGAAGT 1440
QY 1504 AGTTCAAGGCGATATGTTAGTCTTTTAAAGTTGGTTGGGCAATACAGATATGATCGT 1563
DB 1441 AGTTCAAGGCGATATGTTAGTCTTTTAAAGTTGGTTGGGCAATACAGATATGATCGT 1500
QY 1564 AATATATGCTTGAACAGATTAATAATTAATCAATATGATGATCAATTAAGGTTGGGGGGG 1623
DB 1501 AATATATGCTTGAACAGATTAATAATTAATCAATATGATGATGATCAATTAAGGTTGGGGGGG 1560
QY 1624 AATATGCGGTTTGTCAATCCAGGACCTACTGCGGGGGAATTTGGTAAAGTCAAGTATAGT 1683
DB 1561 AATATGCGGTTTGTCAATCCAGGACCTACTGCGGGGGAATTTGGTAAAGTCAAGTATAGT 1620
QY 1684 TGGCATTCATTAAGTTCAAGCAACCAAGACAAACAAAGTTATGATGTTGTTGCGT 1743
DB 1621 TGGCATTCATTAAGTTCAAGCAACCAAGACAAACAAAGTTATGATGTTGTTGCGT 1680
QY 1744 TATGCTTGTATGTTAATCCCATGGGGATGCTATTTTGTATGAAACACAGCGGCAAGTACAT 1803
DB 1681 TATGCTTGTATGTTAATCCCATGGGGATGCTATTTTGTATGAAACACAGCGGCAAGTACAT 1740
QY 1804 ATAGTTTCATTTTGTATGTTGCTCAAAATTCATCAGTCTGTCATCAAAACCTCTTAGAG 1863
DB 1741 ATAGTTTCATTTTGTATGTTGCTCAAAATTCATCAGTCTGTCATCAAAACCTCTTAGAG 1800
QY 1864 AGTGATTTTGGCTATATGATGTTCCAGGATTTTATACACATCAATTAATCCCTTAATA 1923
DB 1801 AGTGATTTTGGCTATATGATGTTCCAGGATTTTATACACATCAATTAATCCCTTAATA 1860
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QY 1924 AGATATAGAACACAAAGCTTTGGTACCCAGCGGATAGCAAAATTGAAATTTCACCTT 1983
DB 1861 AGATATAGAACACAAAGCTTTGGTACCCAGCGGATAGCAAAATTGAAATTTCACCTT 1920
QY 1984 AACACTTTCCGAATCAATCATTTAGAAAAAGAAAGAAAGAAAGTAAATGATCTATTATTC 2043
DB 1921 AACACTTTCCGAATCAATCATTTAGAAAAAGAAAGAAAGTAAATGATCTATTATTC 1980
QY 2044 AATTAA 2049
DB 1981 AATTAA 1986
RESULT 4
AAQ30821
ID AAQ30821 strand; DNA; 3471 BP.
AC AAQ30821;
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 01-APR-1993 (first entry)
XX Toxin 50C.
XX Endotoxin; acarides; pest; Two Spotted Spider; mite; phytophagus; ss.
XX Bacillus thuringiensis; PS50C.
XX MO9219106-A1.
XX 12-NOV-1992.
XX 30-APR-1992; 92MO-US003546.
XX 30-APR-1991; 91US-00693210.
PR 13-SEP-1991; 91US-00759248.
PR 13-SEP-1991; 91US-00768141.
XX (MYCO) MYCOGEN CORP.
XX Payne JM, Cannon RJC, Bagley AL;
PI WPI; 1992-398411/48.
XX P-PSDB; AAR28900.
XX New Bacillus thuringiensis isolates and toxins - used for controlling
PT acarid pests of livestock, fowl, stored prods. and plants.
XX Disclosure; Page 47-48; 62pp; English.
XX Gene sequences encoding a toxin which is active against acarides and is
CC obtainable from B. thuringiensis isolates PS17a, PS17b, 33f2, PSS2A1,
CC PS6901, PS68A1 and PS50C are given in AAQ30803-07 and AAQ30820-21
CC respectively. The toxin is a delta-endotoxin active against acarid pests,
CC including the Two Spotted Spider mite. The isolates can be used against
CC non-phytophagus mites such as acarid pests of livestock, fowl and stored
CC prods. The genes can be cloned and used to transform other hosts, which
CC can be used to control mites, or in the case of transgenic plants, be
CC resistant to mites. (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 24-OCT-2003 to standardise OS field)
CC
XX
SQ Sequence 3471 BP; 1201 A; 567 C; 750 G; 953 T; 0 U; 0 Other;
Query Match 12.5%; Score 256.2; DB 2; Length 3471;
Best Local Similarity 50.5%; Pred. No. 2,9e-49;
Matches 838; Conservative 0; Mismatches 778; Indels 45; Gaps 7;
QY 13 AAAAAATAAATGATATGAAATGTTGGATCTTTCGAATCAACTTAATATGCTTAAT 72
DB 10 AATATATCAAAATGATATGAAATTAATGATGACACACCTTCTACATC--TGATCACT 66

QY 73 TGTATCCAAAGTATTCCTAGCAAAAAGTCCACAAATGACTATGCGAAACAGAACTAT 132
DB 67 GATTTCTACAGATACCCCTTTTGGAATGAGCCAAAGATGCGTTACAAAATATGAAATTAT 126
QY 133 AAGAAATGCTAAATATGATGATCAAAATATACAAATTTATTGGTATTAAGACGAT 192
DB 127 AAGATATATCTGAAATATGCTGGG-----GGAGAAATCTGTAATT 168
QY 193 TCTAGCCCTGAAGCTGCTTTAAGTACAGATGCTGTTTAAACGGATATTAACAGTGA 252
DB 169 TTTGAAATCCGAGACGTTTATTAAGTATCATCAAGATCAAACTGGAATGGCATTTGT 228
QY 253 GGGACTATATCTTTCGAATTTAGGGGCTCTTGGCAAGTCAATCATTTGGAATTAATAG 312
DB 229 GGTGGAATATCTAGAGACTTTAGGGGTTCCATTTGCTAGTACAGATCTGATTTCTAATAG 288
QY 313 AGGCTAATAGTATTTATTTAGGGCAG-----GGCTGATCATTTTAAGCACTTATGTT 366
DB 289 TTGATTTGTTGTCATTTATGCGCGTCAAAAGAGCTGATATATGGGAGAAATTTATGAA 348
QY 367 CTGTGTAAGAGCTTATTTAAGAAAGTATAGTACGCTGTAAAGAAAAATGCTTTAGA 426
DB 349 CGAGTGAAGAACTGTTGATCAAAAATATGAAAAATATGTAAGATTAAGGCTTTGCT 408
QY 427 GAGCTAGAAAGTTTACAGGAAATTTATGACATATATCAAACTAGACTGCAAGATGGCTA 486
DB 409 GAATTTAAAGGCTGGAATATGCTTTGATGATATATCACAGTCACTTGAAGATTTGGCTG 468
QY 487 GTTAACAAGATGATG--ACAATCGAGGAGCCTAGTAACGAGATGCAATTTGTGAT 543
DB 469 GAAATTCGAAATGATGCAAGAACTAGAAATGTTGTTCTAATCAATTTATAGCTTTAGAT 528
QY 544 AACTTTTGAAGAAATATGCAAAATTCGCAAAATTCAGAAAGAACTTTGAAATTTATTTGTA 603
DB 529 CTTAACCTTTGTTAGTTCAATTCATTCATCTTTTGCGATATCCGACACAGAACTATTTATTA 588
QY 604 CCAGTATATGACACAGCCGCAATTTGCAATTTATTTATTTAAGATATGCTGATTTATTT 653
DB 589 GCAATATATGACAGGCTGTGAACCTAATTTATTTATTTAAGATGCTTCTAATTTT 648
QY 664 GGAGCAGATGGCAATTTAGTATGATGATGAAATTCGATTAATTTATTTACAGACTACAAGA 723
DB 649 GAGAGAGATGGGGAATTTACACAGGTGAATTTTCTAGATTTTATATGTCAGAGTCA 708
QY 724 CTGATTAAGAAATATTAAGATCATTTGATTAATGATTTATTAACCAAGGTTTAAATCAATTT 783
DB 709 CTTAACCGTGAATATTTCAACATTTGTTGTAAGTGTATTAATAATCGCTTATTAATTTG 768
QY 784 AATCGTCAAAATGCTCAAAATTTGGTACCTTTAATAGTTTCTGATCAATATGACATTA 843
DB 769 AAGGTACCACTTCAAAAGTTGGCTGAATTTATCATCAGTTCCGTAGAGATGACATTA 828
QY 844 ACAGTATGATCTGCAATATTTATTTTCAAACTATGATCAAGTATGATTCATTAAGCA 903
DB 829 CTGATTTATGATTTTGTGGCGTTATTTCCAAACTATGACACATATGATTCATTCGAA 888
QY 904 GTAAAAACGAAATTTGATGGAAGTTTATACAGATTCAGTATGAGTTTACCTGGGATTTA 963
DB 889 ACAACAGCTCACTTACAGAGGATGATACAGATTCGATGCAATTAACATATGAGACA 948
QY 964 GAAATGAGATGATGATTAACCTTGTGATTAATCTTAATATTAATCAACTTTACTGTAAG 1023
DB 949 AGTACTGATTTCTGCA--ACCTTGTGTACACCACAGTGGTATTTCTTTTATTAAGAGTT 1005
QY 1024 GAAATTAAGCAAGACGAGTCTCTTTATACCACTTGCTTAATGCTATTTTGTATAT 1083
DB 1006 GAAATTAAGCAAGTATTTGTCGCAACCTTTGATATATCTGCTCAGTGAATTAAT 1065
QY 1084 ACAAGGATCTGATTAATATGTT-----CTGATGAGAAATATTTTGGGAGGGCAT 1134
DB 1066 ACAAGTATGAGGGATTTATGTTAATATATGATGATATATATTAACATACGATGTCAGGAT 1125
QY 1135 ACATTAAGTGAAGAAATGATGTTGTTGAATATACCAATACCTTTGGTAAACCTGAT 1194


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Db 1126 ACCCTAAATATGCTAGAAACAGCGTATTCACCGTAACTACACAGCTAATTCAGGTGCA 1185
Qy 1195 TCTATTAATCTCTATTCATATTTTAAATTTGCGCAACCTTCTGTTTCACTATTTAGTCA 1254
Db 1186 ATCACTTCAGAAAGAATTCATTTGCACTTGAGAGATGAGATTTTGGAAATTAATTTCA 1245
Qy 1255 CTGCTCGTATATTTATTTAGAGAGAAACAGAGCTTATATATTTACTAGTCAGTATGA 1314
Db 1246 ACTGTGGCAA---ACCTAGCTAATTAATACCAAAAGGCAATGTGTGCCGGATCTTGG 1302
Qy 1315 GTCTCGAGACTTATTTTAAATACATCAATATTAATTAATGATCTTTAAGATAC 1374
Db 1303 TTCCATATGCTAAAGAGGAGACCTCATCAACACAGCTATTATTAATTCAAAACACAT 1362
Qy 1375 GAAGTCCCTGCTATCTTCATCCCAACATATTAATTAACAATTTACAGAAAGATTAAG 1434
Db 1363 ACAGCTCTCCAAAGGTGTACACAGTTTATGAATCAAGTATGAATACCTCTAGATGA 1422
Qy 1435 CCAGAACCAACGACAGAGATTTCAAGCATATGATTTATCTATATATCAAAATTTTGATGA 1494
Db 1423 ACTGTACCGTACGTAAAGCTATAGTCATAGATTAATCTATTAATCTCCATCTTTC 1482
Qy 1495 CGGCGAAGTATTCAGCGGTATTTGTTAGTCTTTTAAAGTTGTTGGGACATACCAAGT 1554
Db 1483 TCTAAATAGGAGTGAATCTATGGAAGTTTCCCTGATTTTGTGGACATACATAGT 1542
Qy 1555 ATGGAATCGTATATATGCTCTTGAACCGATTAATTAATTAATTAATGATGATTAAGT 1614
Db 1543 GCGGATTTTAAATATATCAATATATTCAGATTAATCACTCAAAATTCAGCGGTAAAGGA 1602
Qy 1615 TGGGGGGGGAATATCGGGTTTGTATCCAGACCTACTGG 1655
Db 1603 GACATGTTATATCTAAGGGGTTCCGTATGATCAAGGCTCTGG 1643

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RESULT 5

AAQ27167
ID AAQ27167 standard; DNA; 3471 BP.

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XX AC AAQ27167,
XX DT 25-MAR-2003 (revised)
XX DT 27-JAN-1993 (first entry)
XX DE Delta-endotoxin gene.
XX KM B.t. PS50C; Colorado potato beetle; Lepidoptera decaemlineata;
XX KM Pseudomonas; expression vector; ss.
XX OS Bacillus thuringiensis.
XX PN EP498537-A2.
XX PD 12-AUG-1992.
XX PF 16-JAN-1992; 92BP-00300366.
XX PR 16-JAN-1991; 91US-00642112.
XX PA (MYCO ) MYCOGEN CORP.
XX PI Fonceerrada L, Sick AJ, Payne JM;
XX DR WPI; 1992-270497/33.
XX DR P-PSDB; AAR25997.
XX PT New insecticidal Bacillus thuringiensis strain NRRL B-18746 - and toxin,
XX PT DNA encoding it, vectors and transformed cells, effective against
XX PT Coleoptera.
XX PS Claim 8; Page 9-11; 16pp; English.
XX

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CC The sequence given encodes an approx. 130 kD protein known as Bacillus
CC thuringiensis PS50C (B.t. PS50C). This novel delta-endotoxin has been
CC shown to be active against the Colorado potato beetle (Lepidoptera
CC decaemlineata). This toxin gene can be transformed into suitable hosts
CC such as Pseudomonas, which can then be applied to the environment of
CC coleopteran insects, where they will proliferate and be ingested by the
CC insects. This sequence can be inserted into an expression vector which
CC contains a promoter/operator region, a ribosome binding site,
CC polyadenylation signals, etc. This will allow transcription and
CC translation of the cells in the appropriate host. (updated on 25-MAR-2003
CC to correct PN field.)

XX Sequence 3471 BP; 1200 A; 567 C; 751 G; 953 T; 0 U; 0 Other;

Qy Query Match 12.5%; Score 256.2; DB 2; Length 3471;

Best Local Similarity 50.5%; Pred. No. 2.9e-49;

Matches 838; Conservative 0; Mismatches 778; Indels 45; Gaps 7;

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Qy 13 AAAAAATGAATATGAAATGTTGATGCTTTACGAATCACTTAATATGCTTAAT 72
Db 10 AATATCAAAATGAATATGAAATTTATAGATGCGACACCTTCTATCCTC---TGATCCAGT 66
Qy 73 TGTATCAAGATATCCACTAGCAAAAAGATCCAAATGACTATGCGAAACAGAACTAT 132
Db 67 GATTTACAGATACCTTTTGCGAAATGAGCCAAAGATGCGTTACAAAATATGAATATAT 126
Qy 133 AAGAAATGGCTAATATATGATGATGATGCAATATTAATGATATTAACAGATAT 192
Db 127 AAGATATATCTGAATATGCTGGG-----GAGAGAAATCTGAAATTA 168
Qy 193 TCTAGCCCTGAAGCTCTTTAAGTATACAGATGCTGTTTAAACGGTATTAACAGTGA 252
Db 169 TTGGAAATCCGAGAGGTTTATAGTATCAACGATTAATCTGAAATATGCAATTTG 228
Qy 253 GCGACTATATCTTCAATTTAGGGGTCCTTTGGCAATCAATCAATTTGGAATATTAAT 312
Db 229 GATCGAATATCTAGAGACTTTTGGGGTTCATTTGCTATGATGATGATGATGATGAT 288
Qy 313 AGGCTAATGATATTTTATGAGGAG-----GGCTGATCATTTGAGCACTTAAGT 366
Db 289 TTCAATGTTGCTAATATATGAGCGGTCAAGAGCGTATGATATGAGGAGAAATTAAGAA 348
Qy 367 CTGTGTAAGAGCTTATTAAGAAATATATGATCAGCGTATAGAGAAATGCTCTTGA 426
Db 349 CGATGGAAGAACTCGTTGATCAAAAATATGAATAATATGAATAAGCTCTTGGCT 408
Qy 427 GACTAGAAAGTTTACAGGAATTAATGATATATCAATATGACTGCAAGATGGCTA 466
Db 409 GAATTAAGAGGCTAGAAATGCTTTGATATATCAGCAGTCACTTGAGATTTGGCTG 468
Qy 487 GTTAACAAGATGATG---ACATCGAGGGCTATGTAACGAGATATGCAATTTGAT 543
Db 469 GAAATATCGAATATCAAGAACTAGAAAGTGTGTTCTAATCAATTTATAGCTTTAGAT 528
Qy 544 AACTTTTCAAAAAGATATGCAAAATTCAGAGAAAGAACTTTGAAATTTTATTTGTTA 603
Db 529 CTTAATCTTTGTTATGTTCAATTCATCTTTTGCGATATCCGAGACAGAAATGATATTA 568
Qy 604 CCAGTATATGACAAACCGGAAATTTGCAATTTATTTATTAAGAGATGCTATATTTT 663
Db 589 GCAGTATATGCAAGAGCTGTAACCTATATTTATTTATTAAGATGCTCTTATATTTT 648
Qy 664 GAGACAGTGGCAATTAAGTATGATGATGAAATTCGATATATTTATCAGACTACAAGGA 723
Db 649 GAGAAAGATGGGATTTTACACAGGTGAATTTCTAATTTATATATGCTCAAGTGCA 708
Qy 724 CTGATTAAGAAATATTAAGATCATTTGATTAATCACTTATACAGAGGTTTAAATCAATTT 783
Db 709 CTTCACCGCTGAATATTCAGACTATTTGTTGTAAGTGTATTAATTCGCTTATGATTAAT 768
Qy 784 AATGCTCAATGCTCAAGATTTGGGTGACCTTATATAGTTTCTGATCAGATATGACATTA 843
Db 769 AAGGTACACCTTCAAAAGTTGGCTGAATTAATCATCATGTTCCGTAGAGATGACATTA 828

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QY 844 AAGATTTAGATCTCGCAATATTATTCCAACTATGATCCAGTAGTATCCATTAGCA 903
 DB 829 CTGGTATTGATTTGGTGGCGTATTATCCAACTATGACACATATGATATCCAACTGAA 888
 QY 904 GTTAAACCGGAATTTGCTAGGGAAGTTTATACAGATCCAGTAGGCTTACTGGGGATTA 963
 DB 889 ACAACGAGCTCACTTACAGCGGATGTGTATACAGATCCGATACCTTATTAACATATGACA 948
 QY 964 GAAAGTAGAGTAGAGCTTACCTTGGTATATCTTATATATCAACTTATCTGCTATG 1023
 DB 949 AGTACTGGATTTGCA---ACCTTGGTCAACCCACAGTGTATCTTTTATGAAAT 1005
 QY 1024 GAAATATACGCAAGACAGCTCTTCTTATACACTTGGTATATGTAAT 1083
 DB 1006 GAAACAGCTATTTGTCGCGACACTTGTGTATATCTGACTGAGTAAATTAAT 1065
 QY 1084 ACAAGACTTAGTAAATATG-----CTGATGTAGAAATTTTGGGAGGGCAT 1134
 DB 1066 ACAAGTAGAGGGGTATACGTAAATATATGATGATATATTAACCTACTGCTACAGACAT 1125
 QY 1135 ACATTAAGTAAATGAAATGATGGTCTGAAATATACCACTTATGTTGGTAAACTGAT 1194
 DB 1126 ACCCTAAATATCTGTAACAGCTGATTTGACCCCTATACATACAGCTAATTCGCTCA 1185
 QY 1195 TCTATTACTCTTATTCATATTTTAAATTTTCGCAACCTTCTGTTTCACTATTTAGTCA 1254
 DB 1186 ATCACTTCAAGAAAGATTCATTTTGGCACTTGAAGATGAGGATATTTTGAATTAATTC 1245
 QY 1255 CTTCCTCTGATATTTTGAAGAGAACAGAGCTATATATTTACTACTGCTATGCA 1314
 DB 1246 ACTGTGCA---ACCTAGCTAATTTACTACAAAGGCAATATGTGTGCGGATCTTGG 1302
 QY 1315 GTCTCGAGATTTTATTTATATCATCAATATATATATGATCTGATCTTAAAGATAC 1374
 DB 1303 TTCCATATGTATTAAGGGAACCTCATCAACAGCGATTTATATTTCAAAACACAT 1362
 QY 1375 GAAGTCCTGCTAATCTTCATCCAACTATATTTATCAGAAATTTACAGAAAGATAG 1434
 DB 1363 ACAGCTCTCAAGAGGTGACAGAGTTTATGATATCAAGTATGAATTAACCTTAGATAG 1422
 QY 1435 CCAAGCAACAGCAGAGATTTTACAGCATATATCTTATATATCAAAATTTGATGCA 1494
 DB 1423 ACTGTACCGGTACTAAAGCTATAGCATATATTTATCTCATTTTACCTCCATTTCTTTC 1482
 QY 1495 CGGCAAGTAGTTCAGGCGGTATTTAGCTTTTAACTTTGGTGGGACATACAGT 1554
 DB 1483 TCTAAATATGGAGTGCATATGGAGTTTCCCTGTATTTTGTGGACATATCTAGT 1542
 QY 1555 ATGATCTGATATATCGTCTTGAACAGATTAATTAATCAAAATAGATGCAATTAAGT 1614
 DB 1543 GCGGATTTAAATATATCAATATATGATATTAATCATCAAAATTCAGGCGTAAAGGA 1602
 QY 1615 TGGGGGGGAATTCGGGTTTGCATCCAGACCTACTG 1655
 DB 1603 GACATGTATATCTAGGGGTTCCGTATGATCAGGGTCTTGG 1643

RESULT 6

AAQ28940 standard; DNA; 3471 BP.

AAQ28940;

24-FEB-1993 (first entry)

B.churingiensis PS50C insecticidal protein gene.

B.t.PS50C; NRRL B-18746; pMYC1638; Colorado potato beetle;

Coleoptera-active toxin; ss.

Bacillus churingiensis.

XX

FH Key Location/Qualifiers
 FT mac_peptide 1..3471
 FT /+tag= a
 FT /product= "toxin"
 FT /note= "active against Coleoptera"

CA2059242-A.

17-JUL-1992.

13-JAN-1992; 92CA-02059242.

16-JAN-1991; 91US-00642112.

02-JAN-1992; 92US-00812180.

(MYCO) MYCOGEN CORP.

Foncerrada L, Sick AJ, Payne JM;

WPI, 1992-323784/40.

P-PSDB; PAR27343.

New Bacillus churingiensis isolate - used for preparing toxin, DNA and transformed hosts for controlling coleoptera insect pests.

Claim 13; Page 18-20; 33pp; English.

PS Total cellular DNA was prepd. from B.t. PS50C. The DNA was partially
 CC digested with Sau3a and 9-23kb fragments were ligated into BamHI-
 CC digested lambda GBM-11. Packaged phage were plated on E.coli KM251 cells
 CC and screened using a radiolabelled probe. Positive plaques were purified
 CC and reseeded. Single isolated purified plaques were used to infect
 CC E.coli KM251 in liquid culture. DNA was isolated, digested with XhoI and
 CC large fragments ligated to XhoI-cut pHTBlueII. The ligation mixt. was
 CC introduced into competent E.coli NM522 cells. Plasmid pMYC1638 contained
 CC a 12kb XhoI insert from which the 3471bp sequence of the toxin gene was
 CC determined

Sequence 3471 BP; 1202 A; 570 C; 745 G; 954 T; 0 U; 0 Other;

Query Match 12.5%; Score 256.2; DB 2; Length 3471;

Best Local Similarity 50.5%; Pred. No. 2,9e+49; Matches 838; Conservative 0; Mismatches 778; Indels 45; Gaps 7;

QY 13 AAAATATTAATGAATATGAATGTTGATGCTTATCGAATCAACTTAATATGCTAAT 72
 DB 10 AATATCAAAATGAATATGAATTAATATGATGCGACCTTCTATC--TGTATCAGT 66
 QY 73 TGTATCAAGATATCACTAGCAAAAGATCCCAAAATGACTATGCGAAACGAACTAT 132
 DB 67 GATTTCAACAGATACCTTTTTCGATGAGCCAAACGATGCTTACAAATATGAATTAAT 126
 QY 133 AAAGATGGCTAAATATGTGTATCAAAATACAAATTAATGATATTAAGCAGTAT 192
 DB 127 AAGATTAATCTGAATATGCTGG-----GGAGAAATCTGAATTA 168
 QY 193 TCTAGCCCTGAAGCTGCTTTAAGTATACAGATGCTGTTTAAACGGTATTAACAGTGA 252
 DB 169 TTTGAAATCCGGAAGACGTTTATATGTTATCATCAAGATTAACAACTGAAATGCAATGTT 228
 QY 253 GGGACTATATCTTCAATTTAGGGGTCCTTTGGCAAGTCATCATTTGGAATTAATAGT 312
 DB 229 GGTGCAATCTAGAGCTTTAGGGGTTTCATTTGCTAGTCAGATACCTGTTTCTATAGT 288
 QY 313 AGGCTAATAGTATTTATGAGGAG-----GGCTGATCATTTTAAGCACTTATAGT 366
 DB 289 TTCATTTGTTGCTAATTAATGCGCGTCAAGAGCGTATATATGAGGAGAAATTAATGAA 348
 QY 367 CTGTTGAAGAGCTTATTAAGAAAGTATAGATCAGCGTATAGAGAAAAATGCTTTAGA 426
 DB 349 CGAGTGAAGAACTGTTTATCAAAAAATATATGTAATAATATAGAGGCTCTTGGCT 408
 QY 427 GAGCTGAAGGTTTACAGGAAATTAATGAGATATATCAAACTAGACTGCAAGATGGCTA 486

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Db      409  GAAATTAAGGAGCTAGGAAATGCTTGGAGTATATACAGACATCTGGAAGATGGCTG 468
Qy      487  GTTAACAAGAAATGATG---ACAATCGAGGGCACTACTAACAAGATGCAATTTGAT 543
Db      469  GAAATTCGCAATGATGCAAGAACTGAAAGTGTGTTCTATCAATTTATGCTTAAAT 528
Qy      544  AACTTTTCCAAAAGAAATATGCGCAAAATTCAGAGAAAGAACTTGAATTTTATGTTA 603
Db      529  CTTAATCTTTGTATGTTCAATTCATCTTTGCAAGTATCCGACACGAAAGTATTTA 588
Qy      604  CCAATATATGCAACAGCCGCAATTTGCAATTTAATTTTAAAGATGCTGATTTT 663
Db      589  GCAATATATGCAACAGCTGTGTAACCTACATTTATTTGATTAAGATGCTTCAATTTT 648
Qy      664  GGAGCAACATGCGCAATTAAGGATGATGAAATTCGTATATTTATACAGATCAAGGA 723
Db      649  GGAGAAAGTGGGGATTTACACAGGTGAATTTCTGATTTTAAATCGTCAAGTCAA 708
Qy      724  CTGATTAAGAAATATTAAGATCATTTGTATTAACATTTATAACAGGTTTAAATCAATTT 783
Db      709  CTTACCGCTGATATTTCAAGATATTTGTATTAAGTGTATTAATCGGCTTATGATTAATG 768
Qy      784  AATCGCTCAAAATGCTCAAGATGCGGTGAGCTTTAATAGTTTCGTACAGATATGACATTA 843
Db      769  AAGGTACACCTCTAATAAGTTGCTGAATATATCATCATGTTCCGTAGAGAGATGACATTA 828
Qy      844  ACAATATTAAGTCTCGCAATTTATTTCCAACTATGATGACATGATATCTTATGCA 903
Db      829  CTGATATTAAGTTGTTGGGGCTTATTTCCAACTATGATGACATGATATGATCAATGAA 888
Qy      904  GTAATAAGCGAATGATGATGAGGAGTTTATATACAGATGAGGTTTATCGGGGTATTA 963
Db      889  ACAACAGCTCACTTACACGAGATGTGTATACAGATCCGATGATTTAATCATAGTACGA 948
Qy      964  GAAAGTGGAGTGAAGATTAACCTTGTGATATATCTAATATACAACTTTACTGCTATG 1023
Db      949  AGTACTGGATTTGCA---ACCTTGGTCAACCAAGTGGTATCTTTTATTAAGAGTT 1005
Qy      1024  GAAATTAACGACAGACAGCTCTTCTTATTAACACTTGGCTTAATCGTATTTTGTATAT 1083
Db      1006  GAAATTAACGATTAATCTGCGCCACACTTGTGATATACACTGACCTGATGAAATTAAT 1065
Qy      1084  ACAAGGCTGATGATATATGCT-----CTGATGGAAGAAATTTTGGGCGAGGCT 1134
Db      1066  ACAAGTGAAGGGGTATTTAGCTTAATATGATGATATTAATTAATCTAGTCTGAGACAT 1125
Qy      1135  ACAATTAAGTGAAGAAATGATGTTCTGAAATTAACCCATTAATCTTGTGAAATGAT 1194
Db      1126  ACCCTTAATAATATCTGATGACAGCTGATTTGCAACGATTAACAGCTAATTAACGCTGA 1185
Qy      1195  TCTATTAATCTCTATTAATTAATTTTGGGCAACCTTCTGTTTCAATGATGATGCA 1254
Db      1186  ATCACTTCAAAAAGAAATTCATTTGCACTGAGGATGAGGATTTTGAATTAATTTCA 1245
Qy      1255  CTTGCTGCTATTAATTTAGAGGAACAGAGCTAATTAATTAATTAATTAATGATGGA 1314
Db      1246  ACTGTGGCAA---ACCTAGCTAATTAATTAATTAATTAATTAATTAATTAATTAATG 1302
Qy      1315  GTCTGAGAGATTTATTTTAAATACATCAAAATTAATTAATTAATTAATTAATTAAT 1374
Db      1303  TTCTCATATGTTAAAGGCAACCTCATCAACAAACAGCTTTTATTAATTAATTAATTAAT 1362
Qy      1375  GAAATGCTGCTAATCTTCAATCCCAAACTAATTAATTAATTAATTAATTAATTAAT 1434
Db      1363  ACAGCTCTCCAAAGGTGATACAGAGTTATGATCAAGATGAAATTAATCTGATAGGA 1422
Qy      1435  CCAAGACCAAAAGGAGATTTGAGCATGATTAATCTTAATTAATTAATTAATTAATTAAT 1494
Db      1423  ACTGTACCGGTAGCTGAACCTATATGATGATTAATTAATTAATTAATTAATTAATTAAT 1482
Qy      1495  CGGGAAGTATGATGAGCGGATTTAGTCTTTTAAAGTTTGGGCAATACAGAT 1554

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Db      1483  TCTAAAAATGGAGTGCATATCTATGGAAGTTTCCCTGATATTTGTTTGACACATACTAGT 1542
Qy      1555  ATGATCGTATATATGCTCTTGAACGATTAATTAATTAATTAATTAATTAATTAATTAAT 1614
Db      1543  GCGATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1602
Qy      1615  TGGGGGGGGAATATCGGTTTGTATCCAGACCTACTGG 1655
Db      1603  GACATGTTATATCTAGGGGGTCCGTATGACAGGCTCTGG 1643

RESULT 7
AA038653
ID  AA038653 standard; DNA; 3471 BP.
XX
AC  AA038653;
XX
DT  25-MAR-2003 (revised)
DT  15-JUL-1993 (first entry)
XX
DE  Bt isolate Pe50C coding sequence.
XX
KM  Lepidopteran-active; toxin; Ti; Ri; plant; cell; Bt; ss.
XX
OS  Bacillus thuringiensis.
XX
PN  MO9304587-A1.
XX
PD  18-MAR-1993.
XX
PF  11-SEP-1992; 92MO-US007697.
XX
PR  12-SEP-1991; 91US-00758020.
PR  08-SEP-1992; 92US-00941650.
XX
PA  (MYCO) MYCOGEN CORP.
XX
PI  Uyeda KA, Bradfish GA;
XX
DR  WPI; 1993-100566/12.
XX
DX  P-PSDB; AAR33768.
XX
PT  Controlling lepidopteran pests - using compsn. of Bacillus thuringiensis
XX  strains or plants or microorganisms transformed with their toxin genes.
XX
PS  Claim 12; Page 20-22; 38pp; English.
XX
CC  The sequences given in AA038653-55 encode lepidopteran-active toxins.
CC  These sequences were used within a T1 or R1 plasmid to transform plant
CC  cells. Whole plants can then be regenerated from the transformed cells.
CC  The toxin may also be produced by cloning Bacillus thuringiensis (Bt).
CC  It may then be applied directly to the plant locus. (Updated on 25-MAR-
XX  2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ  Sequence 3471 BP; 1200 A; 567 C; 751 G; 953 T; 0 U; 0 Other;

Query Match      12.5%; Score 256.2; DB 2; Length 3471;
Best Local Similarity 50.5%; Pred. No. 2.9e-49;
Matches 838; Conservative 0; Mismatches 778; Indels 45; Gaps 7;
Qy      13  AAAAAATTAATGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 72
Db      10  AATTAATCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 66
Qy      73  TGTATCAAGATATCACTAGCAAAAGATCCAAATGATGATGATGATGATGATGATGATGAT 132
Db      67  GATTTAAGATATCACTTTTGGCAATGAGCCAAAGATGCGTTAATAAATTAATTAATTAAT 126
Qy      133  AAGAAATGCTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 192
Db      127  AAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 168
Qy      193  TTAGCCCTGAAGCTGCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 252

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Db 169 TTGGAAATCCGAGACGTTTATTAGTTCACGATTCGAACTGAAATGGCATTTG 228
Qy 253 GGGACTACTTCTGAAATTTAGGGGTCCTTTGGCAAGTCATCATTTGGAAATTAAT 312
Db 229 GGTGCAATCTAGAGACTTTAGGGGTTCCATTGCTAGTCAGATAGTATGTTCTATAGT 288
Qy 313 AGGCTAATAGTATTTTATGGGAG-----GGCCTGATCATTTGAAGCACTTAATGTT 366
Db 289 TTCAATGTTGTCATATTAATGCGCTCAAGAGCGTAGATATATGGGAGAAATTAAGAA 348
Qy 367 CTGTTGAAGAGCTTATTAAGAAAGTATGATCAGGCTTAAGAGAAAATGCTTAGA 426
Db 349 CGAGTGAAGAACTCGTTGATCAAAAAATATGTAATAAGATTAAGGCTCTTGCT 408
Qy 427 GAGCTAAGAGTTTACAGGAAATTAAGACTATATCAAACTAGACGTCAGAGCTGCTA 486
Db 409 GAATTAAGAGGCTTAGAAATGCTTTGATGATATACAGACATCTGAAAGATTTGGCTG 468
Qy 487 GTTAACAGAAATATG---ACAAATCGAGGGGCACTAGTAAAGCATATGCAATTTGAT 543
Db 469 GAAATTCGCAATGATGCAAGAACTAGAAAGTTGTTCTAATCAATTTATAGCTTAGAT 528
Qy 544 AACTTTTGCAGAAAGATATGCCAAATTCAGAGAAAGAACTTTGAAATTTTATTTGTTA 603
Db 529 CTTAACCTTGTGTTCAATTCATCTTTGCAAGTATCCGAGACAGAAATCAATTAATTA 588
Qy 604 CCAGTATATGACAGAGCCGCAATTTGCAATTTATTTTAAAGATGCTGATTAATTT 663
Db 589 GCGATATATGCAAGGCTGTGAACCTACATTTATGTTATTAAGATGCTTATATTTT 648
Qy 664 GGAGCAAGTGGCAATTAAGTATGATGAATAATCGTATATTAATCAAGTACAGAA 723
Db 649 GGAGAAAGATGGGATTTACACAGGTAATTTCTAGATTTATATCTCAAGTGCAA 708
Qy 724 CTGATTAAGAAATTAAGATTCATTTGATTAACATTTCAATTAACAGGTTTAAATCAATTT 783
Db 709 CTTAACGCTGAATATTCAGCTATGTAAGGATTAATAATTCGCTTAGATAATTTG 768
Qy 784 AATCGCTCAATGCTCAAGATTTGGTATGCTTTAATATGATTTGTAAGATATGACATTA 843
Db 769 AAGGATACCACTTTAAAGTTGGCTGAATATCATCATAGTTCCGTAGAGAGATGACATTA 828
Qy 844 ACAGATTAATGATCTCGCAATATTAATTTCAAACTATGATCACAGTATGATTCATTAGCA 903
Db 829 CTGATTAATTAATTTGGTGGCTATATTTCCAACTATGACACATATATGATTCAAATCGAA 888
Qy 904 GTTAAGAAACGAAATTTGACTAGGAAAGTTTATACAGATTCAGTAGGTTTACTGGGATATTA 963
Db 889 ACAACAGCTTCACCTTACACGGAATGATATACAGATCCGATACATTTAACATAGTGACA 948
Qy 964 GAAAGTGAAGTATGAGACTTACCTTGGTATATCTTAATATATCAAACTTTACTGCTATG 1023
Db 949 AGTACTGATTTCTGCA---ACCTTGTGTCACCCACAGTGTATCTTTTATGAAGTT 1005
Qy 1024 GAAATATACGCAAGACGATCTCTTCTTATACACTTGGTTATATGATATTTTGTATAT 1083
Db 1006 GAAATACAAAGCTAATTCGTCGCACTGTTGATATATCTACAGCTCAGTAGAAATTAAT 1065
Qy 1084 ACAAGACTTAGTATATATG-----CTGATGTGAAGAAATTTTGGGAGGGCAT 1134
Db 1066 ACAAGTAGAGGGGTTATTAAGTAAATATATGATGCAATATTAATACTAGTCAAGACAT 1125
Qy 1135 ACATTAAGTGAATGGAATGATGTTTGAATAATACCATTAATCTTTGTTAAACATGAT 1194
Db 1126 ACCCTTAATAATATGTAAGACAGCTGATTCGACCGTAAACATACAGTAAATTCGCTCGA 1185
Qy 1195 TCTATTAATCTTCAATTTTAAATTTTAAATTTGCGAACTTTCTGTTTCAGATATGAGTCA 1254
Db 1186 ATCACTTCAAGAAAGAAATTCATTTGCACTTGAAGATAGGATATTTTGAATAATTAATTC 1245
Qy 1255 CTGCTCTGATATATTTAGAGGAAACAGAGGCTAATATTAATTAATTTACTAGTACGTATGCA 1314

Db 1246 ACTGTGGCAA---ACCTACTAATTACTACCAAAAGCAATATGTTGCGGATCTTGG 1302
Qy 1315 GTCTCGAGATTAATTTTATATACATCAATATATATATGATCTGATCTTTAAGATAC 1374
Db 1303 TTCCATATGATGAATAAGGGAACTTCATCAACAGACCGATATTAATTAATCAAAAAACAT 1362
Qy 1375 GAAGTCCCTGCTAATTTTCCATCCCAACTATATTAATCAAGATTTACCAGAAAGTAAAG 1434
Db 1363 ACAGCTCTCCAAAGGATGTCACAGGTTTATGATCAAGTAAATACCTTAGATAGA 1422
Qy 1435 CCAGAACCAACGACAGAGATTTACAGCATATGATTAATTTATCAAAATTTGATGCA 1494
Db 1423 ACTGTACCGGATGCTAAGATCTATAGTCAATATTTATCAATTTCTCCCATTTCTTC 1482
Qy 1495 CCGCGAAGTATGTTACAGCGGATATTTGATCTTTTAACGTTGGTGGCACATACAGT 1554
Db 1483 TCTAATAATGGGAGTGCATATGATGAGAGTTTCCCTGTATTTGTTGACACATTAAGT 1542
Qy 1555 ATGATCTGATTAATATGTTGTTGAACCAATTAATAATTAATCAATATGATGATTAAGT 1614
Db 1543 GCGGATTTAATAATTAATCAATATATTCAGATTAATAATCACTCAAAATTCACGCGTAAAGGA 1602
Qy 1615 TGGGGGGGAATATGCGGTTTGTATCCAGGACCTACTGG 1655
Db 1603 GACATGTTATATCTAGGGGCTTCCTGATGTAAGGGTCTGG 1643

RESULT 8
AAT43222
ID AAT43222 standard; DNA; 3471 BP.
XX
AC AAT43222;
XX
DT 16-OCT-2003 (revised)
DT 28-JAN-1997 (first entry)
XX
DE Antiscarab pest toxin 50C(a) coding sequence.
XX
KW Toxin 50C(a); scarab pest; toxin; insect; scarabaeidae; pest control;
KW larval stage insect; grain; tuberous crop; white grub; chafer grub;
KW cyclocephala; popillia; ds.
XX
OS Bacillus thuringiensis; strain kumamocensis.
XX
PN US554534-A.
XX
PD 10-SEP-1996.
XX
PE 30-SEP-1994; 94US-00315468.
XX
PR 16-DEC-1991; 91US-00808316.
PR 30-JAN-1992; 92US-00828430.
PR 01-FEB-1993; 93US-00014941.
XX
PA (MYCO) MYCOGEN CORP.
XX
PI Foncerrada L, Narva KE, Michaels TE;
XX
DR WPI; 1996-424659/42.
XX
DR P-PSDB; AM06418.
XX
PT New nucleic acid encoding B. thuringiensis toxin active against scarab(s)
PT - also related toxin and transformed microbes, effective against adult
PT pests and their larvae.
XX
PS Example 2; Col 17-20; 24pp; English.
XX
CC AAT43221-743221 represent the coding sequences for toxins that are active
CC against scarab pests. This sequence was isolated from the Bacillus
CC thuringiensis strain kumamocensis. Insects in the family Scarabaeidae
CC constitute a serious pest control problem, especially when destructive
CC larval stage insects infest high value turf found in golf courses,
CC playing fields and lawns. The larvae of many species also attack grains,

CC tuberous crops, and ornamentals. The larvae are known as white grub, or
CC chaffer grubs, and can be found in decaying organic matter, or in the soil
CC where they consume plant roots. In Europe and the U.S. populations of
CC these larvae and adults have developed resistance to chemical
CC insecticides such as the organochlorines and DDT. The toxins encoded by
CC these sequences, and intact cells that are capable of expressing the
CC proteins, can be used to control many pests of the family scarabaeidae,
CC such as species of Cyclocephala, and Popillia. The toxins are active
CC against larvae (present in soil) and against adults. (Updated on 16-Oct-
CC 2003 to standardise OS field)

Sequence 3471 BP; 1200 A; 567 C; 751 G; 953 T; 0 U; 0 Other;

Query Match	12.5%	Score 256.2	DB 2	Length 3471
Best Local Similarity	0.5%	Pred. No. 2.9e-49		
Matches 838, Conservative	0	Mismatches 778	Indels 45	Gaps 7

Qy	13	AAAAATAAAATGATATGAAATGTTGGATGCTTTACGAATCAACCTCAATATGCTAAT	72
Db	10	AATATATCAAAATGATATGAAATATATAGTGGACACTTCAACATC---TGATATCACT	66
Qy	73	TGTTATCCAGGATATCCACTAGCAAAAGATCCAAATGACTATGCGAAACGAACTAT	132
Db	67	GATTCATAACAATACCTTTTGCGAATGAGCCAAAGATCGGTCAAAATATGAAATAT	126
Qy	133	AAAGAAATGGCTAAATATNGTGTATCAATATACAATTTATGTGATATAGCACTAT	192
Db	127	AAAGATTATCGAAAAATGCTGGG-----GGAGAGATCTTGATTA	168
Qy	193	TCTAGCCCTGAAGCTCTTAAAGTATACAGAGATCGTGTTTAAACGGGTATTAACAGTGA	252
Db	169	TTTGGAATATCCGAGACGTTTATTAAGTTCATCCACGATTCAAACCTGGAAATGGCAATGTT	228
Qy	253	GGACATATACCTTTCGAATTTAGGGGTCCCTTTGGCAAGTCAATCAATTGGAAATTAAGT	312
Db	229	GGTGAATATCATAGAGACTTTAGGGGTTCCATTTGTAGTCAATATAGCTTATTAATG	288
Qy	313	AGGCTAATAGGATTTTATATGGGCA-----GGCGTATCCATTTGAAGCACTAATAGTT	366
Db	289	TTCAATGTTGGTCAATATATGCGCTCAAGACGTAAGATATATGGGAGAAATTAATGAA	348
Qy	367	CTTGTGGAAGACTTATTTAAGAAAGATATAGTACGCGTGAAGAAAGAAATCTCTTACA	426
Db	349	CGAGTGAAGAACTGTTGATCAAAAATATAGAAAATATGTAAAGATTAAGCTCTTGCT	408
Qy	427	GAGCTAAGAGTTTACAGGGAATATAGACTATATCAAACTAGACTGCACATGGCTTA	486
Db	409	GAAATTAAGAGGCTAGGAATGCTTTGGATGTATATACGACGTCACTGMAATATGGCTG	468
Qy	487	GTTAACAAGATGATG---ACAATGGAGGGCACTAAGTAAAGCAGATGCAATGTGTAT	543
Db	469	GAAATGCAATGATGCAAGAACTAGAAAGTGTGTTTCTAATCAATTTATAGCTTTAGAT	528
Qy	544	AACTTTTGCAAAAGAAATATGCAAAATTCAGAAAGAAACTTTGAATTTATGTGA	603
Db	529	CTTAACCTTGTATGTTCAATTCATCTTTTGCAGATATCGAGACAGAAATCTATTAATTA	588
Qy	604	CCAGTATATGCAACAGCCGCGCAATTTGCAATTTATTTATTAAGAGATGCTGATATTTT	663
Db	589	GCAGTATATGCAACAGGCTGTGAACCTCAATTTATGTATTAAGAGATGCTTCTATTTT	648
Qy	664	GGAGCAACAGTGGCAATTAGTGATATGAAATTTGCGATAAATTAATATGCACTACAGGA	723
Db	649	GGAGAAAGATGGGATTTACACACAGTGAAATTTCTAGATTTTATATATGCTCAAGTCAA	708
Qy	724	CTGATTAGAGAAATATAAAGATCATTTGTATACATTCATATACAGAGTTTAAATCAATTT	783
Db	709	CTTACCGCTGATATTCAGACTATTTGTGTAAGTGTATAAATCGGCTTAATTAATTTG	768
Qy	784	AATGCTCAAAATGCTCAAGATTTGGGTGAGCTTAATAGTTTCTGATCAAGATATGCAATTA	843
Db	769	AAAGGTACACTTCTAAAGATGGCTGAATTTATCATCAAGTTCCTGAGAGATGACATTA	828

Oy	844	CAAGATTAAGATCTCGAAATATTAATTTCCAAACATATATCCACGTAGATATCCATTAGCA	903
Db	829	CTGGTATTAGTTTGGTGGCTTATTTCCAAACTATGACACACATATGATTCCAATGGA	888
Oy	904	GTAAAAACGGAATTAGCTAGGGAAGTTTATACAGATCCAGTAGGGTTTACTGGGGTATTA	963
Db	889	ACAAACAGCTCACTTACACGGGAGTGTATACATATCCGATAGCATTTAAACATAGTACA	948
Oy	964	GAAATGAGGTAGGACTTACCTTGGTATTAATCTTAATAATACACCTTACTAGCTATG	1023
Db	949	AGTACTGGATTCTCA--ACCTTGGTCAACCAAGTGGTATTTCTTTTATGAAGTT	1005
Oy	1024	GAATAATACGCAACGACGCTCTTCTTATACACTTGGCTTATTCGTATTTTGTATAT	1083
Db	1006	GAATAACAGTAAATTCGTCCGCCACACTTGTGTATATCTACACTCAGTACGAATAATAT	1065
Oy	1084	ACAGAGACTTAGGTAAATATGT-----CTGATGTGAAATTAATTTGGGGAGGGCAT	1134
Db	1066	ACAAAGTAGAGGGGTATTACGTTAAATATGATGCATATATTAACCTAGTCCAGGCAT	1125
Oy	1135	ACATTAGTGAATAATGAATAATGATGTTCTGAATAACCAATTAACCTTGGTAAACATGAT	1194
Db	1126	ACCTTAAATATGCTAGAACAGCTGATTTGACGCTAACATACAGCTAATTAACGTCGA	1185
Oy	1195	TCTATTACTCTTATTCATATTTTAAATTTATTTGCGAACCTTCTGTCTTCAATTAGTCA	1254
Db	1186	ATCATCTCAGAAAAGAAATTCATTGGCACTTGAGATAGGGATATTTTGAATAATTAATCA	1245
Oy	1255	CTTGCTGATATATTTTACGAGAACAGAGGCTATTAATTAATTTACTAGTCAATGGA	1314
Db	1246	ACTGTGGCAA---ACCTAGCTAATTACTACCAAAAGGCATATGTGTGCGGGATCTTGG	1302
Oy	1315	GTCCTCGAGAGTTATTTTAAATACATCAAAATATTAATATGATACCTGGATCTTTAAGATAC	1374
Db	1303	TTCCATATGTGTAATAAAGGGAACCTCATCAACAAACAGCATTATTAATTCAAAAACAT	1362
Oy	1375	GAAGTGCCTGCTAATCTTCATCCCAACTATATTAATCAAGATTACAGAAAGATTAAG	1434
Db	1363	ACACCTCTCCAAAGGTGTACACAGGTTTATGAAATCAAGTATGAATAACCTAGATAGA	1422
Oy	1435	CCAAAGACAAACGAGAGATTTCAAGCATATGATTAATCTTAATATGCAATTTTGATGCA	1494
Db	1423	ACTGTACCGGTAGCTGAAGCTATAGTCATAGATTAATCTCAATATTAATCTCCATCTTTC	1482
Oy	1495	CGAGGAAGTAGTACGCGGATATGTAGTCTTTAATAGTTTGGTGGGCACATACCAGT	1554
Db	1483	TCTAAATATGGAGATGCATACTATNGGAAGTTTCCCTGTATTTGTTGGACACATACAGT	1542
Oy	1555	ATGATCGTAAATATCGTCTTGAAACAGATPAAATTAATCAATATGATGCAATTAAGGT	1614
Db	1543	GCGGATTTAAATATATACAAATATATTCAGATAAATATCACTCAAATTCACAGCGGTAAAGGA	1602
Oy	1615	TGGGGGGGAAATATCGGGTTTGTATCCCAAGAACCTATCTGG	1655
Db	1603	GACATGTTATATCTAGGGGGTTCCGTATGACAGGGTCTTGG	1643

RESULT 9	
AAQ51704	
ID	AAQ51704 standard; DNA; 3471 BP.
XX	
XX	
AC	AAQ51704;
XX	
XX	
DT	24-OCT-2003 (revised)
DT	25-MAR-2003 (revised)
DT	09-DEC-1995 (first entry)
XX	
DB	Bacillus thuringiensis cryetal protein PS50C gene.
XX	
KM	Cryetal protein; delta endotoxin; acaricide; pesticide;
KM	biological control agent; transgenic plant; crop improvement; ds.
XX	
DS	Bacillus thuringiensis serovar kumamotoensis; (isolate PS50C).

Db	1543	GC	GAGATTTAAATTAATACATATATATACAGATTAATAATCACTCAAAATTCGACGGTAAAGGGA	1643
Qy	1615	TC	GGGGGGGGGAATATCGGGTTGTATCCACGAGCACTTACTGG	1655
Db	1603	GAC	ATGTTATATCTAAGGGGCTTCGCTAGTACAGGGTCTCTGG	1643
RESULT 10				
ABKS1132				
ID	ABKS1132	standard; cDNA; 3690 BP.		
XX	ABKS1132;			
AC				
XX				
DT	30-JUL-2002	(first entry)		
XX				
DE	cDNA encoding <i>Bacillus thuringiensis</i> insecticidal protein.			
XX				
KM	Insecticide; transgenic; coleoptera larvae; ss; gene.			
XX				
OS	<i>Bacillus thuringiensis</i> .			
XX				
XX	Key	Location/Qualifiers		
FT	CDS	187..3690		
FT		/*tag= a		
FT		/product= "Insecticide protein"		
XX				
PN	JP2002045186-A.			
PD	12-FEB-2002.			
XX				
PF	03-AUG-2000; 2000JP-00236140.			
XX				
PR	03-AUG-2000; 2000JP-00236140.			
XX				
PA	(SDSB-) SDS BIOTECH CORP.			
XX				
WP	WPI; 2002-356466/39.			
DR	P-PSDB; AAU80281.			
XX				
PT	A protein having insecticidal activity, a DNA encoding said protein, and			
PT	an agent and a method for preventing harmful organisms.			
PS	Claim 4; Page 17-18; 19pp; Japanese.			
XX				
CC	This invention relates to a crystalline protein comprising a fully			
CC	defined sequence and the nucleotide sequence encoding this protein. The			
CC	protein of the invention is an agent for preventing harmful organisms			
CC	comprising <i>Bacillus thuringiensis</i> serovar galleriae SDS502, its mutant or			
CC	a microbe transformed by a DNA encoding the protein. This microbe can be			
CC	used to produce a protein containing the protein, or containing a protein			
CC	having insecticidal activity produced by the SDS502, its mutant or a			
CC	transformed microbe, a microbe which is transformed by using the above			
CC	DNA and produces the above protein having insecticidal activity, a plant			
CC	or a seed transformed by using the above DNA, and <i>Bacillus thuringiensis</i>			
CC	serovar galleriae SDS502 producing a protein comprising and producing a			
CC	protein showing insecticidal activity. The protein of the invention may			
CC	have insecticidal activity. The agent is used for preventing Coleoptera			
CC	larvae. This sequence represents the cDNA encoding the <i>Bacillus</i>			
CC	<i>thuringiensis</i> insecticide protein of the invention			
XX				
XX	Sequence 3690 BP; 1289 A; 599 C; 762 G; 1040 T; 0 U; 0 Other;			
Qy	Query Match	11.5%; Score 236; DB 6; Length 3690;		
Db	Best Local Similarity	55.9%; Pred. No. 1.5e-44;		
Matches	546; Conservative	0; Mismatches 400; Indels 30; Gaps 4;		
Qy	13	AAAAATAAATAATGAATGAATGTTGGATGCTTTACGAATCACTTAATATGCTAAT	72	
Db	196	AATATATCAAAATGAATATGAATATCTATGATGCTTCATCATCTA---CTTCGTATCCGAT	252	
Qy	73	TGTTATCCAGATATCCACTGACGAAAGATCCACAAATAGATCTATGCGAAACGAAATAT	132	
Db	253	AATTCCTGTTAATATACCTTTTGACAAACGATCAACGACACATATTCAGAAACATGAATAT	312	

Oy	133	AAAGAATGGCTAATATGTGTGATTTCAAAATACACAAATTTATTTGGTGTATATAGACGAT	192
Db	313	AAAATATATCTCGAATAATGCTAG-----GGAGGAATCCTGAATTA	354
Oy	193	TCATGCCCTGAAGCTGCTTTAAGTATACGAGATGCTGTTTTAAACGGGTATTAAACATGTA	252
Db	355	TTTGGAAATCCGGAGACGTTTATATAGTTCAATCTACGGTTCAAACTGGAAATGGCATTTGT	414
Oy	253	GGGACTATACCTTTGAAATTNAGGGGTCCCTTTGGCAAGTCATATTTGGAAATTAATAGT	312
Db	415	GGTCAAGTACTGGGGGCTTTAGGGGTTCATTTGGCTGACAGATAGCTAATTTTATAGT	474
Oy	313	AGGCTAATAGGATTTTATGGGCGAGGGCC-----GATCATTTTGAAGCATTTAGGTT	366
Db	475	TTCTATGTCGGTCAATTTATGGCCATCAAGTACCGTGAGTGTATGGGAAATGATTAATGAA	534
Oy	367	CTTGTGTGAAGAGCTTATTTAAGAAAAGTATAGATCAGCGTGTAAAGAAAATGCTTTAGA	426
Db	535	CAAGTGGAAAGTCTAATTTGATCAAAAATAACAGATTTCTGTAAGAAAACAGGCTTGCA	594
Oy	427	GAGCTAAGAGTTTACAGGGAATTAAGACTATATCTAACTAGACTGCAAGCATGGCTTA	486
Db	595	GGACTACAGAGATTAGAGATGCGTTAGACGTATATAGAAATCATCTTAAGAAATGGCTG	654
Oy	487	GTTAACAAGATGATGACA---ATCGGAGGGCACTAGTAACGCGTATGCAATTTGATAT	543
Db	655	GAAATATGTATATGATACAAAGACTAGAGTGTGTGGTGACCCAAATATATAGCTTTAGAG	714
Oy	544	AACTTTTCGAAAAGAAATATGCCAAAATTCAGGAAAAGAACTTTGAATTTTATTTGTTA	603
Db	715	CTTGAATTTTGTGTCTAATAATCCCATCTTTGCAATATCTGGAACGAAAGTACCATTTATTA	774
Oy	604	CCAGTATATATGACAAAGCCGGGAATTTGCATTTAATTTAATAGATAGTGCATTAATTT	663
Db	775	TCAGTGTATGACAAAGCAGGGAATTTACATTTGCTATATATTAAGAGATGCTTCATTTT	834
Oy	664	GGAGCAGAGTGGCAATTAGGATGATGAATTCGTATATTTATCATCACTACAGACAAGA	723
Db	835	GGAGCAGAGTGGGATTCACACACAGGAAATTTCCACATTTATATGATTCGTACAGTGACA	894
Oy	724	CTGATTAGAGATATTAAGATCATTTGTATTAACATTTCTATTAACAGGCTTTAAATCAATTT	783
Db	895	CGTACCCGCCCAATCTCGGATTAATTTGTGTAAAGGTGATTAACACTGGCTTAGATTAATTTA	954
Oy	784	AATGGCTCAATGCTCAAGATTTGGGTGACCTTTAATAGTTTGSTACAGATATGACATTA	843
Db	955	AAAAGTACGAATGTGCAAGTTGGCTGAAGTATCCAAATTCGMAAGAAATGACATTA	1014
Oy	844	ACAGTATTTAGATCTCGCAATATTTATTTCCAAACTATGATCCACGTATGATTCATTTAGCA	903
Db	1015	CTGTATATTAAGATTTAGTAGCTTAATTTCCAAACTATGACACAGTACGTATTCATGGA	1074
Oy	904	GTAATAAAACGAATTTAGCTAAGGAAATTTATACAGATCCAGTACGAGGTTTACTGGGTAATTA	963
Db	1075	ACAACGGCCCACTTACACGGGAAAGTATATACAGATCCATATGATTTTAAACAGGAACA	1134
Oy	964	GAAAGTGGAGGTAGGA 979	
Db	1135	AGTGTGATTTTGTGA 1150	

KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
 XX insect target range; endotoxin; Cry12i8; gene; da.
 OS *Bacillus thuringiensis*.
 XX MO200234774-A2.
 PN
 XX
 PD 02-MAY-2002.
 PF 24-OCT-2001; 2001WO-US045468.
 XX
 XX 24-OCT-2000; 2000US-0242838P.
 PR 23-OCT-2001; 2001US-00032717.
 XX
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA
 XX
 XX Abbad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
 PI WPI; 2002-519178/55.
 DR P-PSDB; AAU99257.
 XX
 XX New isolated pesticidal polypeptide useful for impacting insect pest e.g.
 PT Colorado potato beetle.
 PS
 XX
 XX Claim 1; Page 106-108; 176pp; English.
 CC The present invention relates to a new pesticidal polypeptide. The
 CC invention is useful for impacting an insect pest by applying the by
 CC molecules of the invention to the environment of the insect pest by
 CC spraying, dusting, broadcasting, or seed coating, where the insect pest
 CC is selected from Colorado potato beetle, western corn rootworm or
 CC southern corn rootworm. The invention is also useful for increasing
 CC insect target range and for producing transgenic microorganisms and
 CC plants that express the pesticidal polypeptide. The invention is also
 CC useful for producing transformed plants and in transforming any organism
 CC to produce the pesticidal polypeptide of the invention. The present
 CC nucleic acid sequence encodes a *Bacillus thuringiensis* wild-type Cry12i8
 CC endotoxin protein
 CC
 XX
 XX Sequence 2003 BP; 686 A; 348 C; 392 G; 577 T; 0 U; 0 Other;
 SO
 Query Match 11.5%; Score 235.6; DB 6; Length 2003;
 Best Local Similarity 56.5%; Pred. No. 1.5e-44;
 Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;
 QY 13 AAAAAATAAATGAATGTAATGATGATGCTTTACGAATCAACTATATATGCTTAAT 72
 DB 10 AATTAATCAAAATGAATATGAAATTAATATGATGCGACACCTTTA---CTTGTATCAAT 66
 QY 73 TGTATCCAAAGTATCCACTAGCAAAAGATCCAAATGACTATGCAAAACAGAACTAT 132
 DB 67 GATTCTAACAGATACCTTTTGGCAATGACCAAAATGCGCTAACAAATATGATTTAT 126
 QY 133 AAGAATGCTAATATGTGTGATTCAAATACACATTTATGTGTATATACACATAT 192
 DB 127 AAGATATATTTAAATAATGTCGGGGAATGCTAGTAATACCTGGTTCA----- 177
 QY 193 TCAGCCCTGAAGCTGCTTAAGGTATCGAGATGCTGTTTAAACGGGTATTAACAGTAT 252
 DB 178 -----CTGAAATTAATCTGTTAGCGCAAGATGCACTAAGCCGCAATTTGATATAGTA 231
 QY 253 GGAATTAATCTTTCGAATTTAGGGGTCCTTTGGCAAGTCATCATTTGGAAATATTAAT 312
 DB 232 GGTAAATTAATCAAGTTTAAAGGGGTCATTTGTTGGGCGATAGATGATCTTTATAC 291
 QY 313 AGGCTAATAGTATTTTATGAGGCAAGGCGCTGA-----TTCATTTGAGCACTTAATG 366
 DB 292 CAATTAATGATATTTCTGTGGCCCTTCAGGGGAAAGATCAATGCAAAATTTTATGGA 351
 QY 367 CTGTGTAAGAGCTTATTAAGAAAGATAGATCAGGCTATAGAGAAATGCTTTAAG 426
 DB 352 CAATGAAAGAACTATTAATCAAAAATAGCAAGATATGCAAGAAATTAAGCGCTTTG 411

QY 427 GAGCTGAAAGGTTTACAGGAAATTTATGAGACTATATCAAACTAGACTGCAGATGGCTA 486
 DB 412 GAATTAAGAAAGATATGATATATTAATCAATTAATCTAATGCGCTTGAAGAAAGGAA 471
 QY 487 GTTAACAAAGATAGATGACAATGAGAGGCACTAGT--AAGCAGATGCAATTTGTTAT 543
 DB 472 GAAATCCAAATGTTTCAAGAGCCTTACGAGATGTGCGAAATGCAATTTGAAATCTGGA 531
 QY 544 AACTTTTGGAAAGAAATATGCGAAATTTCAAGAAAGAACTTTGAAATTTTATTTGTTA 603
 DB 532 AGTTTATTTAAGCAATATATATGCAATCTTTTAAAGTACAAATTTTAAAGTACATTCCT 591
 QY 604 CCAATATATGACACAGCCCGCAATTTGCAATTTTATTTTAAAGATGCTGATTTATTTT 663
 DB 592 ACTGATATATGCAATGAGCAGCCCAACCTTCAATTTTAACTGTTTAAAGGACCGCTCA 651
 QY 664 GGAGCACTGTGCAATTAATGATGATGAATTCGATATTAATATATACACTACAAGGA 723
 DB 652 GGAGAAAGATGGGAGATGTCACCAACTACTATTAATTAATTAATATGATGCTCAATGAAA 711
 QY 724 CTGATTAGAAATATTAAGATCATTTGATATATACATTTATACCAAGGTTTAAATCAATTT 783
 DB 712 CTTACTGCAAGAAATATTTCTGATCAGCTGTAAAGTGTATGAAACGTGTTTACCAATATTA 771
 QY 784 AATCGCTCAAAATGCTCAAGATTTGGTGAGCTTTATATAGTTTCGTAACATATGACATTA 843
 DB 772 AAGGACGACGAGGCTTAACCAATGAGTTGACTATTAACCAATTCGTTGAGAAATGACACTG 831
 QY 844 ACAGATTAATGATCTGCAATATTTTCCAACTATATGATCCAGTAGATCCATTAGCA 903
 DB 832 GCGGTTTATGATGTTGTTTCATTTATTTCCAAATTAATGACACAGCGACGCTAACCAATGGA 891
 QY 904 GTAAAAACGAAATTTGCTAGTGAAGTTTATACAGATCCAGTAG 947
 DB 892 ACGAAAGCACTAACAAGGAGATATATACAGATCCACTGGG 935
 RESULT 12
 ABR87241
 ID ABR87241 standard; DNA; 2010 BP.
 XX
 XX ABR87241;
 AC
 XX 07-OCT-2002 (first entry)
 DT
 XX
 XX *Bacillus thuringiensis* Cry12i8-1A truncated gene sequence.
 DE
 XX
 XX Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;
 KW Colorado potato beetle; western corn rootworm; southern corn rootworm;
 KW insect target range; endotoxin; Cry12i8; gene; da.
 XX
 OS *Bacillus thuringiensis*.
 XX
 PN MO200234774-A2.
 PD
 XX
 XX 02-MAY-2002.
 PF 24-OCT-2001; 2001WO-US045468.
 XX
 XX 24-OCT-2000; 2000US-0242838P.
 PR 23-OCT-2001; 2001US-00032717.
 XX
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA
 XX
 XX Abbad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;
 PI WPI; 2002-519178/55.
 DR P-PSDB; AAU99262.
 XX
 XX New isolated pesticidal polypeptide useful for impacting insect pest e.g.
 PT Colorado potato beetle.
 PS Claim 1; Page 123-125; 176pp; English.

XX The present invention relates to a new pesticidal polypeptide. The
 CC invention is useful for impacting an insect pest by applying the
 CC molecules of the invention to the environment of the insect pest by
 CC spraying, dusting, broadcasting, or seed coating, where the insect pest
 CC is selected from Colorado potato beetle, western corn rootworm or
 CC southern corn rootworm. The invention is also useful for increasing
 CC insect target range and for producing transgenic microorganisms and
 CC plants that express the pesticidal polypeptide. The invention is also
 CC useful for producing transformed plants and in transforming any organism
 CC to produce the pesticidal polypeptide of the invention. The present
 CC nucleic acid sequence encodes a *Bacillus thuringiensis* wild-type Cry1218
 CC endotoxin protein

XX Sequence 2010 BP; 690 A; 348 C; 394 G; 578 T; 0 U; 0 Other;

Query Match 11.5%; Score 235.6; DB 6; Length 2010;
 Best Local Similarity 56.5%; Pred. No. 1.5e-44;
 Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

13 AAAAATAAATGAATGAATGTTGGATGCTTACGAATCACTGTAATATGCTAAT 72
 10 AATATCAAAATGAATGAATATGATGCGACACCTCTA--CTTCTGATCCAAAT 66
 73 TGTATCAAGATTCACCTAGCAAAAGATCCACAAATGACTATGCGAAACGACAT 132
 67 GATTCTAACAGATACCTTTTGGCAATGAGCCAAATATGCGCTACAAATATGATAT 126
 133 AAAGATGGCTAAATATGATGATTCAAATACAAATTAATGATATAGACATAT 192
 127 AAAGATTAATTAATAATGTCGCGGAAATGCTAGTAATACCTGGTTCA----- 177
 193 TCTAGCCCTGAGAGCTCTTAATGATGTAAGATGCTGTTTAAAGGGATTAACAGTGA 252
 178 -----CCTGAGAGTCTGTTAGCGACAAAGATGAGTAAAGCGCAATGATATGTA 231
 253 GGGACTATCTTGAATTTAGGGGTCCTTTGGCAATCAATGATTTGGAATATTAGT 312
 232 GGTAAATCTATCAGGTTTAGGGGTCCCATTTGTGGCGGATGATGAGCTTTATATCT 291
 313 AGGCTAATAGTATTTATGCGGAGGCGCTGA-----TCCATTTGAACATTAATGCTT 366
 292 CAATTAATGATATCTGTGGCTTTCAGGGGAAAGATCAATGGAAATTTTATGAAA 351
 367 CTGTGTAAGGCTTATTAAGAAAGATATAGATCAGCTGTAAGAAAGAAATGCTTATAGA 426
 352 CAATTAAGAAATCTATTAATCAAAAATAGCAAAATATGCAAGAAATTAAGCGCTTTCG 411
 427 GAGCTAAGGTTTACAGGAAATATGAGACTATATCAACTATGACATGCAAGATGGCTA 486
 412 GAATTAAGAGATTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 471
 487 GTTAAACAAGATGATGACAAATCGAGGGCACTAGT--AAGCGATATGCAATTTGTTGAT 543
 472 GAAATTCAAATGCTTCAAGAGCTTACAGATGCGAAATCAATTTGAAATCCTGGAT 531
 544 AACTTTTTCGAAAGATATGCCAAATTCAGAGAAAGAACTTTGAAATTTTATGTTA 603
 532 AGTTATTTTACGCAATATATGCCATCTTTAGAGTGAAGAAATTTTGAATGCCATTCCTT 591
 604 CCAATATATGCAAGAGCGGAAATTTGCAATTAATTTATTAAGAGATGATATATTTT 663
 592 ACTGTATATGCAATGCGACGCACTTCAATTTACTGTTATTAAGAGCGCTCAATTTT 651
 664 GGAGCAGAGTGGCAATTAAGTATGATGAATTCGTGTAATTAATTAATTAATTAATTAAT 723
 652 GGAAGAAATGGGATGCTCAACAACATCTATTAATACTATTAATGATCGTCAATGAAA 711
 724 CTGATTAAGAAATTAAGATCATTTGTTAATCAATTTCAACGGGTTTAAATCAATTT 783
 712 CTTACTGAGAAATTTCTGATCAGCTGTGTAAGAGTGAAGACTGGTTTGAACAAATTA 771
 784 AATGCTCAAAATGCTCAAGATTTGGGTGAGCTTTAATAGTTTCGTAAGATATGACATTA 843

DB 772 AAAGCAGAGCGGTAAACAATGGTGTGACTATTAACCAATTCGTAGAAATGACACTG 831
 QY 844 ACAGATTAATGATCCGCAATATTAATTTCAAACTATGATCAGTAGATTCCTTATGCA 903
 DB 832 GCGGTTTATGATGTTGTTGCAATTTTCCAAATTAATTAACACAGCAGTACCAATGGA 891
 QY 904 GTAAAAACGAAATTAAGTGAAGAAATTTATATACATGATCCAGTAGG 947
 DB 892 ACGAAGCAGACATTAACAGGAAATGATATATACATGATCAGTGGG 935

RESULT 13

ADL15314
 ID ADL15314 standard; DNA; 2010 BP.

AC ADL15314;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE B thuringiensis strain 1218 Cry1218-1 (Cry8Bb1) truncated DNA.

XX endotoxin; proteolytic site; insect gut; pesticidal; agriculture;
 KW plant pest; Cry8-like delta-endotoxin; Cry1218-1; Cry8Bb1; ds; gene.
 XX *Bacillus thuringiensis*.

PN W02004003148-A2.

PD 08-JAN-2004.

PP 25-JUN-2003; 2003MO-US020027.

XX 26-JUN-2002; 2002US-0391786P.

PR 04-APR-2003; 2003US-0460787P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

PA Abad AR, Flanagan RD, Herrmann R, Kahn TW, Lu JL, McCutchen BF;
 PI Presnell JK, Wong JFH, Yu C;

XX WPI; 2004-083033/08.

DR P-PSDB; ADL15315.

XX New endotoxin comprising a mutation consisting of the alteration of at
 PT least one proteolytic site, where stability of the endotoxin in insect
 PT gut is increased, useful for providing improved pesticidal activity.

XX Example 4; SEQ ID NO 11; 333pp; English.

XX The invention relates to a novel endotoxin having a mutation consisting
 CC of the alteration of at least one proteolytic site, where the stability
 CC of the endotoxin in an insect gut is increased relative to an endotoxin
 CC lacking the mutation. The endotoxin of the invention may be useful for
 CC providing improved pesticidal activity against insect pests whilst the
 CC compositions of the invention may be useful in agriculture for
 CC controlling pests, including plant pests. The current sequence is that of
 CC the DNA related to *Bacillus thuringiensis* strain 1218 Cry8-like delta-
 CC endotoxin Cry1218 of the invention.

XX Sequence 2010 BP; 690 A; 348 C; 394 G; 578 T; 0 U; 0 Other;

Query Match 11.5%; Score 235.6; DB 12; Length 2010;
 Best Local Similarity 56.5%; Pred. No. 1.5e-44;
 Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

13 AAAAATAAATGAATGAATGTTGGATGCTTACGAATCACTGTAATATGCTAAT 72
 10 AATATCAAAATGAATGAATATGATGCGACACCTCTA--CTTCTGATCCAAAT 66
 73 TGTATCAAGATTCACCTAGCAAAAGATCCACAAATGACTATGCGAAACGACATAT 132
 67 GATTCTAACAGATACCTTTTGGCAATGAGCCAAATATGCGCTACAAATATGATATAT 126

```

QY 133 AAGAAATGCTAATAATGTGTGATTCATAATACCAATTATGTGTATTAACAGCTAT 192
   |||
   |||
Db 127 AAGATTAATTAATAATGCTGCGGGAATGTATGATTAACCTGGTCA----- 177
   |||
QY 193 TCTAGCCCTGAACTGCTTTAAGTATCGAGATGCTGTTTAAACGGTATTAACAGTGA 252
   |||
Db 178 -----CCTGAAGTACTGTTGTAGCGGCAAGATGCAAGCTTAAGCCGCAATGTATAGTA 231
   |||
QY 253 GGGACTATACCTTCGAATTTAGGGGTCCTTTGGCAAGTCAATCATTTGGAAATTAATAGT 312
   |||
Db 232 GGTAAATTAATCAAGTTTAAAGGTCCTCAATTTGTTGGCCGATAGAGATCTTTATCT 291
   |||
QY 313 AGGCTAATAGTATTTTATGAGGAGGCGCTGA-----TCCATTTGAAGCACTTAATGTT 366
   |||
Db 292 CAACCTATTGATATTCGTGCGCTTCAGGGGAAAGAGATCAATGGGAAATTTTATAGAA 351
   |||
QY 367 CTGTGTGAAGAGCTTATTAAGAAAAGTATGATCAGGCTTAAGAAAATGCTTTAGA 426
   |||
Db 352 CAAGTGAAGAACTCATTAATCAAAAATAGCAAGAAATATCAAGAAATTAAGCGCTTTCG 411
   |||
QY 427 GAGCTGAAGAGTTTACAGGAATTAATGAGCTATATCAACTAGACTGCAAGATGGCTA 486
   |||
Db 412 GAATTAAGAGATTAAGTATTAATTAATACCAATTAATTAATCTGCGCTTGAAGATGGAA 471
   |||
QY 487 GTTAACAAGATATGACAAATCGAGGGCACTAGT--AACGAGTATGCAATTTGTTAT 543
   |||
Db 472 GAAATATCAAAATGTTTCMAAGCCTTACAGATGTGCGAAATGCAATTTGAATTCCTGAT 531
   |||
QY 544 AACTTTTTCGAAAAGAAATATGCCAAATTCAGAGAAAAGAACTTTGAAATTTTATGTTA 603
   |||
Db 532 AGTTTATTTTACGCAATATATGCAATCTTTTGAAGTGAAGAAATTTTGAAGTCAATTCCT 591
   |||
QY 604 CCAGTATATSCAAGAGCCGCAATTTGATTTAATTTTATTAAGAGATGCTGATTTATTT 663
   |||
Db 592 ACCTATATGCAATGCGAGCAACCTTCAATTTACTGTTATTAAGACGCGTCAATTTT 651
   |||
QY 664 GGAGCAAGTGCATTTAGGTGATGATGAATAATTCGTGATTAATTAATCAGACTACAGAA 723
   |||
Db 652 GGAGAAATATGGGATGTGTCACAACTACTATTAATTAATTAATGATCGTCAAAATGAAA 711
   |||
QY 724 CTGATTAAGAAATTAAGATTCATTTGATTAACATTCATTAACAGGTTTAAATCAATTT 783
   |||
Db 712 CTTAATGCGAATAATTTCTGATCACTGTGAAGTGGATGAATACTGTTTGAAGAAATTA 771
   |||
QY 784 AATCGCTCAATGCTCAAGATTTGGTGAAGCTTTAATAGTTTGTGACAGATATGACATTA 843
   |||
Db 772 AAAGGACGAGCGCTTAACATATGGTTGACTATTAACCAATTCGCTAGAGAAATGACACTG 831
   |||
QY 844 ACAGTATTAATCTCGCAATTAATTTCCAACTATGATCCAGCTAGATGATTCATTAAGCA 903
   |||
Db 832 GCGGTTTATGATGTGTTGATTAATTCCTCAATTAATGACACAGCAGTACCAATGGA 891
   |||
QY 904 GTAAAAACGAATTGACTAGGGAAGTTTATACAGATCCAGTAGG 947
   |||
Db 892 ACGAAAGCACTAATCAACAGGAAATATATACAGATCCACTGGG 935
   |||

```

RESULT 14

ABE45616
ID ABE45616 standard; DNA; 2010 BP.

XX ABE45616;

XX 22-SEP-2005 (first entry)

XX B. thuringiensis Cry toxin, Cry12Ib-1 (truncated), DNA.

XX Toxin; de; gene; transgenic plant; insecticide; pesticide;

XX plant insect pest; Cry8.

XX Bacillus thuringiensis; strain 1218-1.

OS Synthetic.

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XX PN WO2005066349-A2.
XX XX
XX PD 21-JUL-2005.
XX XX
XX PF 09-DEC-2004; 2004MO-US041530.
XX XX
XX PR 24-DEC-2003; 2003US-00746914.
XX XX
XX PA (PION-) PIONEER HI-BRED INT INC.
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX XX
XX PI Abad A, Dong H, Herrmann R, Lu A, Mccutchen BF, Rice JA;
XX PT Scheperle EJ, Wong JF;
XX DR WPI; 2005-533612/54.
XX DR P-PSDB; ABE45617.
XX XX
XX PT Novel isolated nucleic acid molecule having nucleotide sequence encoding
XX PT pesticidal polypeptide comprising engineered proteolytic protection site
XX PT resistant to protease, useful for protecting plant from pest e.g.
XX PT Colorado potato beetle.
XX XX
XX PS Example 4; SEQ ID NO 11; 362bp; English.
XX XX
XX CC The invention relates to an isolated nucleic acid molecule comprising a
XX CC nucleotide sequence encoding a pesticidal polypeptide having an
XX CC engineered proteolytic protection site, which is not sensitive to the
XX CC plant protease and protects the pesticidal polypeptide from proteolytic
XX CC inactivation in a plant. Also included are protecting (M1) a pesticidal
XX CC polypeptide from proteolytic inactivation in a plant (comprising altering
XX CC a proteolytic site within the pesticidal polypeptide that is sensitive to
XX CC a plant protease to comprise a proteolytic protection site, where the
XX CC proteolytic protection site is not sensitive to the plant protease and
XX CC protects the pesticidal polypeptide from proteolytic inactivation in a
XX CC plant), an expression cassette (II) comprising the nucleic acid, a
XX CC transformed plant (III) a stably incorporated with the expression
XX CC cassette in its genome, a transformed seed of the plant and an isolated
XX CC pesticidal polypeptide (IV) having proteolytic activity (and comprising
XX CC an engineered proteolytic protection site, which is not sensitive to the
XX CC plant protease and protects the pesticidal polypeptide from proteolytic
XX CC inactivation in a plant). The pesticidal polypeptide is Cry8Bb1 toxin or
XX CC its variant or fragment, where the variant and the fragment have
XX CC pesticidal activity and the variant has at least 70 % sequence identity
XX CC to an amino acid sequence for the Cry8Bb1 toxin. The nucleic acid and/or
XX CC expression cassette are useful for protecting a plant from a pest, where
XX CC expression of the nucleic acid and/or expression cassette in the plant
XX CC produces the pesticidal polypeptide in the plant, and where the
XX CC pesticidal polypeptide protects the plant from the pest. The plant
XX CC protease is a cysteine protease. The pest is chosen from Colorado potato
XX CC beetle, Western corn rootworm, Southern corn rootworm, and boll weevil.
XX CC The present sequence encodes a truncated Bacillus thuringiensis Cry8-1like
XX CC toxin, described in the examples section of the specification.
XX XX
XX SQ Sequence 2010 BP; 690 A; 348 C; 394 G; 578 T; 0 U; 0 Other;

```

Query Match 11.5%; Score 235.6; DB 14; Length 2010;

Best Local Similarity 56.5%; Pred. No. 1.5e-44;

Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

```

QY 13 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 72
   |||
Db 10 AATTAATCAAAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 66
   |||
QY 73 TGTATCAAGATATCACTAGCAAAAGATCCCAATATGACTATGCGAAACAGCACTAT 132
   |||
Db 67 GATTCTAACAGATATCCCTTTTGGCAATGACCAACAAATCGCTATCAAAATATGATTAAT 126
   |||
QY 133 AAGAAATGCTAATAATGTGTGATTCATAATACCAATTTATGTGTATTAAGACAGCTAT 192
   |||
Db 127 AAGATTAATTAATAATGCTGCGGGAATGTATGATTAACCTGGTCA----- 177
   |||
QY 193 TCTAGCCCTGAACTGCTTTAAGTATCGAGATGCTGTTTAAACGGTATTAACAGTGA 252
   |||

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Db      178 -----CTGAAAGTACTTGTTCACGCGACAAAGATGCAAGCTTAAGCCGCAATATGATATAGTA 231
QY      253 GGGAGCTATATCTTGAATTTAGGGGGTCCCTTGGCAAGTCAATCATTTGGAAATATAGT 312
Db      232 GGTAAATTTACTATCAGGTTTAGGGGGTCCCTTGGGGCCGATGAGTACTTTTATACT 291
QY      313 AGGCTAATAGTATTTTATGGGCGAGGCTGA-----TCCATTTGAGCACTTATGTT 366
Db      292 CAATCTATTGATATTTCTGTGGCCCTTCAGGGGAAAGATCAATGGGAAATTTTATAGAA 351
QY      367 CTGTGTAAGAGCTTATTAAGAAAGATATGATCAGCTGTAAAGAAAATGCTCTTGA 426
Db      352 CAAGTAGAAGACTCTTATTAACAAAATAGCAAAATATGCAAGATTAAGAGCGCTTTCG 411
QY      427 GAGCTAAGAGCTTACAGGGAATTAAGACTATATCAAACTAGACCTGCAAGAGCTCTA 486
Db      412 GAATTAAGAAAGATTAAGTAAATTAATCAATTAATCTGCGCTTGAAGAAATGGAA 471
QY      487 GTTAAACAAAGATGATGACATCGGAGGCACTAGT---AAGCAGTATGCAATGTTGAT 543
Db      472 GAAATTCCAAATGCTTCAAGAGCTTACGAGATGTGGAATGATTTGAAATCCTGGAT 531
QY      544 AACTTTTTCGAAAAGATATGCCAAAATTCAGGAAAGAACTTTGAAATTTATTTGTTA 603
Db      532 AGTTTATTTACGCAATATATGATCCATCTTTAGAGTGAATTTGAAATGATCCTT 591
QY      604 CCAGTATATGCAACAGCCGGAATTTGATTTATTTATTAAGATGCTGATATTTT 663
Db      592 ACTGTATATGCAATGCGACCACTTCAATTTCTGTATTAAGAGCGGTCATTTTTT 651
QY      664 GGAGCAGTGGCAATAGGTGATGATGAATTCGTATTAATTAATCAGACTACAAAGA 723
Db      652 GGAGAAAGATGGGATGTCAACACTATCTATTAATCTATTTATGATGCTCAATGAAA 711
QY      724 CTGATTAAGAAATATTAAGATCAATTTGATTAACAATCTATAACAGGGTTTAAATCAATTT 783
Db      712 CTTAAGTCAATATTTCTGATCACTGTGTAAGGATGATGAAATCTGTTTATGCAAAATTA 771
QY      784 AATCGCTCAATGTCTCAAGTTGGGTGAGCTTTATATAGTTTGTATGATATGACATTA 843
Db      772 AAAGGACGAGCCCTAAACAAATGGGTGACTATTAACCAATTCGTAGAGAAATGACACTG 831
QY      844 ACAGTATTAATCTCGCAATATTTATTCAAACTAGATCCAGTATGATGATTCATAGCA 903
Db      832 GCGGTTTATGATGTTGTCATTTATTCCTCAATTTATGACACAGCAGCTACCAATGGA 891
QY      904 GTAAAAACGGAATGACTAGGGAAGTTTATATACAGATCCAGTAGG 947
Db      892 AGCAAAACACACTAACAAAGGAAGTATATACAGATCACTGGG 935

```

RESULT 15

AAT43221 standard; DNA; 3507 BP.

```

ID      AAT43221
AC      AAT43221;
XX      16-OCT-2003 (revised)
DT      28-JAN-1997 (first entry)
XX      Antiscarab pest toxin 50C(b) coding sequence.
DE      Antiscarab pest toxin 50C(b) coding sequence.
XX      Toxin 50C(b); scarab pest; toxin; insect; scarabaeidae; pest control;
KM      larval stage insect; grain; tuberous crop; white grub; chafer grub;
XX      cyclocephala; popillia; db.
OS      Bacillus thuringiensis; strain kumamotoensis.
XX      US5554534-A.
XX      10-SEP-1996.
XX
XX

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PF      30-SEP-1994; 94US-00315468.
XX
XX      16-DEC-1991; 91US-00808316.
PR      30-JAN-1992; 92US-00828430.
PR      01-FEB-1993; 93US-00014941.
XX
XX      (MYCO) MYCOGEN CORP.
XX      Fonceirada L, Narva KE, Michaels TE;
XX      WPI: 1996-424659/42.
DR      P-PADB; AAM06417.
XX
XX      New nucleic acid encoding B. thuringiensis toxin active against scarab(s)
PT      - also related toxin and transformed microbes, effective against adult
PT      pests and their larvae.
XX
XX      Claim 2; Col 27-30; 24pp; English.
XX
XX      AAT43221-T43223 represent the coding sequences for toxins that are active
CC      against scarab pests. This sequence was isolated from the Bacillus
CC      thuringiensis strain kumamotoensis. Insects in the family Scarabaeidae
CC      constitute a serious pest control problem, especially when destructive
CC      larval stage insects infest high value turf found in golf courses,
CC      playing fields and lawns. The larvae of many species also attack grains,
CC      tuberous crops, and ornamentals. The larvae are known as white grubs, or
CC      chafer grubs, and can be found in decaying organic matter, or in the soil
CC      where they consume plant roots. In Europe and the U.S. populations of
CC      these larvae and adults have developed resistance to chemical
CC      insecticides such as the organochlorines and DDT. The toxins encoded by
CC      these sequences, and intact cells that are capable of expressing the
CC      proteins, can be used to control many pests of the family Scarabaeidae,
CC      such as species of Cyclocephala, and Popillia. The toxins are active
CC      against larvae (present in soil) and against adults. (Updated on 16-OCT-
CC      2003 to standardise OS field)
XX
XX      Sequence 3507 BP; 1256 A; 576 C; 732 G; 943 T; 0 U; 0 Other;
SQ

```

Query Match 11.5%; Score 235.6; DB 2; Length 3507;

Best Local Similarity 56.5%; Pred. No. 1,8e-44; Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

```

QY      13 AAAAAATGAATATGAAATGATGATGCTTTACGAATCACTTAATATGCTTAAT 72
Db      10 AATATCAAAATGATATGAAATATATATGATGACACCTTCTATC--TGTATCAAT 66
QY      73 TGTATTCGAAGTATCCACTAGCAAAAGATCCCAATGACTTGGAAACAGAACTAT 132
Db      67 GATTTCAACAGATACCTTTTGGAAATGAGCCAAACAAATGCGTTACAAATATGATTA 126
QY      133 AAGAAATGGCTAATATATGATGATTAACAATTAATTTGATATTAAGCAGTAT 192
Db      127 AAGATTAATTTAAATATGCTGCGGAAA-----TGTATGAAATACCT 171
QY      193 TCTAGCCCTGAAGCTCTTAAAGTATACGAGATGCTTTTAAACGGTATTAACAGTAT 252
Db      172 GCTTACCTGAGTATTTCTTAAGCAAGATGAGTATTAAGCCCAATATGATATAGTA 231
QY      253 GGGACTATACCTTGAATTTAGGGGTCCTTGGCAAGTCAATCATTTGGAATATTAAT 312
Db      232 GGTAAATTTACTAACAGATTTAGGGGTTCATTTGTTGGCCGATGAGTCTTTTATCT 291
QY      313 AGGCTAATAGTATTTTATGGGCG-----AGGCGCTGATCCATTTAGACACTTATGTT 366
Db      292 CAATTAATGATATTTCTGTGGCCCTTCAAAACAAAGATCAATGGGAAATTTTATAGAA 351
QY      367 CTGTGTAAGAGCTTATTAAGAAAGATATGATCAGCTGTAAAGAAAATGCTCTTGA 426
Db      352 CAAGTAGAAGACTCTTATTAACAAAATAGCAAAATATGCAAGATTAAGAGCGCTTTCG 411
QY      427 GAGCTAAGAGCTTACAGGGAATTAAGACTATATCAAACTAGACCTGCAAGAGCTCTA 486
Db      412 GAATTAAGAAAGCTTAAAGTAAATTAATCAATTAATCTGCGCTTGAAGAAATGGAA 471

```

```
QY 487 GTTACAGATGATGATGCAATCGAGGGCACTAGT--AAAGCATATGCAATGTTGAT 543
Db 472 GAAATATCCAAATGATTCAGAGACCTTACGAGATGTTGCAATGATTTGAAATCTGGAT 531
QY 544 AACTTTTGGAAAAAGATATGCCAAATTCAGAGAAAGAACTTTGAAATTTTATTTGTA 603
Db 532 AGTTTATTTAGGCAMATATATGATGATCTTTGAGTGCAGCAATTTTGAAATGACCATTCCTT 591
QY 604 CCAGTATATGCACAGACCGGCAATTTGATTTTATTTTATTTATTAAGAGATGCTGATTTATTTT 663
Db 592 ACAGTATATACAAATGGCAGCAAACTTACATTTTATTTATTAAGGAGCATCATTTT 651
QY 664 GGAGCAGATGGCAATTAAGTGTGATGAAATTCGTGATATTTATATCAGACTACAGGA 723
Db 652 GGAGAGAAATGGGGAATGCTTACAGACACTATTAATTACTATATATCGTCAAAATGAAA 711
QY 724 CTGATTAGAGATATTAAGATCATTTGATTAACATTCATTAACAGAGTTTAAATCAATTT 783
Db 712 CTTACTGCAGAAATATCTGTGACCACTGTGTAAGTGTATGAAACTGTGTTAGCAAAATTA 771
QY 784 AATCGCTCAAAATGCTCAAGATTGGGTGAGCTTTAATAGTTTGTACAGATATGACATTA 843
Db 772 AAAGCTTCGAGCGCTAAACAATGATGACTATTAACCAATTCCTAGAGAAATGACATTG 831
QY 844 ACAGTATTAATGATCTCGCAATATTTTCCAACATATGATCCACGTAGATATTCATTAGCA 903
Db 832 ACGGTGTAGACGTTGTGATTAATTTTCAAACTATGATACGCGTACGTATCCACTGGCA 891
QY 904 GTAAAAACGGAATTGACTAGGGAAGTTTATACAGATCCAGTAGG 947
Db 892 ACAACAGCTCAGCTTACAAAGGAAGTATATACAGATCCACTTG 935
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Search completed: December 24, 2005, 13:41:38
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OM nucleic acid - nucleic search, using SW model

Run on: December 24, 2005, 12:19:38 / Search time 7454 Seconds
(without alignments)
12861.112 Million cell updates/sec

Title: US-10-782-096-1
Perfect score: 2049
Sequence: 1 atgactcattacataaaataa.....atgactcattacataaa 2049

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: gb_esc1:*
2: gb_esc2:*
3: gb_esc3:*
4: gb_esc4:*
5: gb_esc5:*
6: gb_esc6:*
7: gb_esc7:*
8: gb_esc8:*
9: gb_esc9:*
10: gb_esc10:*
11: gb_esc11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	3.0	1101	10	CNS0039G
2	56	2.7	1101	10	CNS0039G
3	53.2	2.6	1101	10	CNS0039G
4	52.8	2.6	575	9	BZ780846
5	52.8	2.6	928	10	CNS000DY
6	52.6	2.6	844	10	BK139987
7	51.6	2.5	1101	10	CNS0182P
8	50.8	2.5	1101	10	CNS000E7
9	50.6	2.5	856	10	AG544460
10	50.4	2.5	707	10	CG403581
11	49.4	2.4	1001	10	CNS0155H
12	49.2	2.4	657	9	B54873
13	49.2	2.4	1110	1	AJ925976
14	49	2.4	989	10	CNS028A4
15	48.4	2.4	886	10	CZ239945
16	48.4	2.4	889	10	CM973509
17	48.2	2.4	1110	10	CM939551
18	48	2.3	1085	10	CNS012AK
19	47.8	2.3	1146	10	CNS02162
20	47.6	2.3	540	3	BP049165
21	47.6	2.3	1101	10	CNS014XJ
22	47.2	2.3	806	11	CNS04ABE

C 23	47.2	2.3	888	9	AZ550737	AZ550737 ENTGA48TF
C 24	47.2	2.3	893	9	AZ680121	AZ680121 ENTMB94TF
C 25	47.2	2.3	1134	10	CL110320	CL110320 ISB1-53F3
C 26	47	2.3	602	10	CZ597892	CZ597892 OM_Ba004
C 27	47	2.3	976	11	CNS04E5M	AL286627 Tetraodon
C 28	46.8	2.3	471	10	CG807194	CG807194 118078H0
C 29	46.8	2.3	602	11	DR7024T	AL735588 Danio rer
C 30	46.8	2.3	670	9	BZ388480	BZ388480 EINDL2TF
C 31	46.8	2.3	781	10	BX145762	BX145762 Danio rer
C 32	46.6	2.3	587	9	BH873429	BH873429 hp45a07.b
C 33	46.6	2.3	734	10	CNS01OMP	AL099163 Drosophila
C 34	46.6	2.3	948	10	AG044370	AG044370 Pan trogl
C 35	46.6	2.3	1101	10	CNS003BD	AL064091 Drosophila
C 36	46.6	2.3	1201	10	CNS015Z2	AL106121 Drosophila
C 37	46.4	2.3	594	3	BJ393609	BJ393609 BJ393609
C 38	46.4	2.3	1101	10	CNS000E7	AL069440 Drosophila
C 39	46.4	2.3	1101	10	CNS0106X	AL098895 Drosophila
C 40	46.2	2.3	641	9	AQ946120	AQ946120 Sheared D
C 41	46.2	2.3	1101	10	CNS016LT	AL106856 Drosophila
C 42	46	2.2	1101	10	CNS00FVE	AL071238 Drosophila
C 43	45.8	2.2	506	3	BM276457	BM276457 PFEST0a8
C 44	45.8	2.2	536	3	BM275822	BM275822 PFEST0a8
C 45	45.8	2.2	764	6	CA856291	CA856291 PFEST0a2

ALIGNMENTS

RESULT 1
CNS0039G/c 1101 bp DNA linear GSS 03-JUN-1999
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly). genomic survey sequence.

ACCESSION
AL063921 GI:4941778
VERSION
AL063921.1 GI:4941778
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS
TITLE
JOURNAL
Genoscope.
Direct Submission.
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazuhiro Oosawa and
Aaron Mammoxer in Peter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR08K10"
/clone_1b="RPCI-98"
/note="end : TET3"

ORIGIN

RESULT 3
CNS017KE/c 1101 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC
DEFINITION BACN37F11 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL108152
VERSION AL108152.1 GI:5628456
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyroidae; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLES Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
JOURNAL BF 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.
FEATURES
source Location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN37F11"
/clone_1b="DrosBAC"
/plasmid="pBelobAC11"
/note="end : T7"

ORIGIN
Query Match 2.6%; Score 53.2; DB 10; Length 1101;
Best Local Similarity 35.1%; Pred. No. 0.11;
Matches 184; Conservative 73; Mismatches 258; Indels 9; Gaps 1;
Query 926 AAGTTATACAGATCCAGTGGGTTTCTGGGGATTAGAAAGAGGTTAGCACTTACC 985
Db 651 AAKKAAGKTCAGACACAKAATAAAGGCKKGGKDAAPAAAPAKKAAPAKKAKKAKK 592
Query 986 CTGTATATATCTTAATATATACCACTTTATCTGCTATGAAATTAACGAAGCAGCTC 1045
Db 591 KKAAGKAAAKKDKCBAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 532
Query 1046 CTTCCTATACCACTTGGCTTAATCGTATTTTGTATATACAGAGCTTAGTAA---- 1100
Db 531 TTGKWCAGKATTAAGAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 472
Query 1101 -----TATGTCGATGCGAATAATTTGGGAGGCGCTATAGTTGAAATGGAATG 1156
Db 471 ATTAAATGTTTTTGTATTTATTTTATTTTATTTATTTATTTATTTATTTATTTAA 412
Query 1157 ATGCTCTGAATTAACCATTAACCTTGGTAAACGATGCTTATTAATCTTATTCATATT 1216
Db 411 ATTATTTGAATTAATAAGTATTTTATTTATTTATTTATTTATTTATTTATTTAAK 352
Query 1217 TTAATTTGGGAACTTTCTGTTTTCAGATGATGCTGCTGATATATTTAGAG 1276
Db 351 WAAWAAWAAWTTAAWAAWTAATTTATTTTAAAGTTTTTTTTTTTWTATTAATAT 292
Query 1277 GAACAGAGGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1336
Db 291 AAATTAAATTAATTAAT 232
Query 1337 CATCAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1396

RESULT 4
BZ780846 575 bp DNA linear GSS 14-MAR-2003
LOCUS BZ780846
DEFINITION 1120h11.g1 WGS-SbicolorF (DH5a methyl filtered) Sorghum bicolor
ACCESSION BZ780846
VERSION BZ780846.1 GI:28958388
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 575)
REFERENCE Rabinowitz, P.D., O'Shaughnessy, A.L., Ballja, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zlatavern, T., Palmer, L., McComble, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Sorghum bicolor (methyl-filtered) Unpublished (2002)
COMMENT Contact: W. Richard McComble
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccomble@cshl.org
Plate: 1120 row: h column: 11
Seq primer: -21M13UnivRev
Class: shotgun
High quality sequence stop: 575.
FEATURES
source Location/Qualifiers
1..575
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="1120h11"
/lab_host="DH5a"
/clone_1b="WGS-SbicolorF (DH5a methyl filtered)"
/note="Site 1: Xba I; Site 2: Xba I; The vector was digested with Xba I and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (Xba I/Xba I) reads in M13mp19, into DH5a."

ORIGIN
Query Match 2.6%; Score 52.8; DB 9; Length 575;
Best Local Similarity 46.7%; Pred. No. 0.12;
Matches 168; Conservative 0; Mismatches 192; Indels 0; Gaps 0;
Query 992 ATATATCTAATATTAACAACCTTACTGCTATGAAATTAACGAAGCAGCTCTTCT 1051
Db 198 ATATCTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 257
Query 1052 ATACACTTGGCTTAATCGTATTTTGTATATACAAAGACTTAAAGTATATGTCGATG 1111
Db 258 ATATATCTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 317
Query 1112 TGAGAAATATTTGGGAGGCGACATTAAGTGAATGGAATGATGCTTGAATTA 1171
Db 318 ATATATATCTACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 377
Query 1172 CCATTAACCTTGGTAAACGATTTCTATTAATTAATTAATTAATTAATTAATTA 1231

[illegible]

OY		1341	AATATAAATTAAAGTACCTGACTGCCTTAAGAATXCGGAAGTCGTCAATCCTCATCCCA	1400
Dd		659	AAAAAAAAAAAAAAAATAAAAAATTTTAAABAATBAABAAAAAATTAAWTTTTTTTTTT	718
OY		1401	AACTATATTATACGAATTACCAGGAAGATTAAGCCAACAACCAAACGACAGATTTCAG	1460
Dd		719	TTTTATTTWMAATATAMAATATMTWMAMTWTDGMKNMNNANNAWWWWWMAAWMAAA	778
OY		1461	CCATAGTTTATCTTATATATCAAAATTTTGATNGCACGGSCGAAGTAGTTCAGCGGATATGT	1520
Dd		779	WWWWWWWWWWMAAAAAAAAAAAAAAAAAAMDDDDDDMMKAKKKKKKKKKKKKK	838
OY		1521	TAGCTTTTAACGTTTGG	1538
Dd		839	KKKKBGGKTKKTITTTKG	856
RESULT 6		BX139987	844 bp DNA linear GSS 13-MAR-2003	
LOCUS		BX139987	Danio rerio genomic clone DKEX-99E7, genomic survey sequence.	
DEFINITION		BX139987		
ACCESSION		BX139987.1	GI:27971314	
VERSION		GSS:		
KEYWORDS		Danio rerio (zebrafish)		
SOURCE		Danio rerio		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE		Actinopterygii; Neopterygii; Teleostei; Ostariophysi;		
AUTHORS		Cypriniformes; Cyprinidae; Danio.		
JOURNAL		I (bases 1 to 844) Humphrey,S.J., Huckle,E. and Durham,J.L. Direct Submission Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished This sequence was generated from the T7 end of BAC 99E7_99E7 is part of the Dariokey HAC Library created by R. Plasberk and N.V. Keygene. Further details: http://www.sanger.ac.uk/projects/D_rerio/ .		
FEATURES		location/Qualifiers		
source		1..844 /organism="Danio rerio" /mol_type="genomic DNA" /db_xref="taxon:7955" /cclone="DKEX-99E7" /rname="Teatlie8" /note="Vector plindigobac-536"		
ORIGIN				
Query Match		2.6% Score 52.6; DB 10; Length 844; Best Local Similarity 46.6%; Pred. No. 0.15; Matches 169; Conservative 0; Mismatches 194; Indels 0; Gaps 0;		
OY		992 ATATCTATTAATCAACCTTAAGCTAGTAAATPAAACGCAAGACGCTCTT	1051	
Dd		441 ATAATTAATTAATGATPAATDAATGAATATATTAATTAATGATPAATTAATATG	500	
OY		1052 ATRACACTGGCTTAATCGTATTTTGTATATACAAAGACTAGTAAATGTCTGATG	1111	
Dd		501 ATAATATTGATGATPAATPAATDAATGATATATTAATTAATGATPAATTAATGATA	560	
OY		1112 TGAGAAATPTTTGGGGAGGCCATTCATTAGTTGAAAAATGCAATGATGCTTGAATPA	1171	
Dd		561 ATAATTAATTAATTAAGATPAATPAATTAATGATGATTAATTAATGAATGATTAATGATA	620	
OY		1172 CCCATACCTTGGTGAAGAGATTCATTAATCTCTTAATTCATATTTTAATTTCCGAACC	1231	
Dd		621 ATAATTAACAATTAATTAATTAATGATTAATTAATTAATGATGATPAATTAATTAATA	680	
OY		1232 TTTCCTGTTTCAGATTAGAGTCACTTCTCGATATATTAGAGAGAACAGAGCTAATA	1291	
Dd		681 ATATATGATGATTAATTAATTAATGATTAATGATTAATGCAATTAATTAATGATCAATTAATA	740	

QY 1292 ATTATATCTAGTCACTAGTCAAGTCTCGAGACTTATTTTAAATACATCAATATATAA 1351
DB 741 ATATATATATATGAT 800
QY 1352 ATG 1354
DB 801 ATG 803

RESULT 7
CNS0182P 1101 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION BACN37D10 of Drosophila library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL108811 GI:5629115
VERSION GSS.
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (BDGP) -
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billand at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobac11.

FEATURES
source location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN37D10"
/clone_lib="DrosBAC"
/plasmid="pBelobac11"
/note="end : SP6"

ORIGIN
Query Match 2.5%; Score 51.6; DB 10; Length 1101;
Best Local Similarity 20.5%; Pred. No. 0.27;
Matches 117; Conservative 209; Mismatches 241; Indels 5; Gaps 1;
QY 408 AAGAGAAATGCTCTTAGAGAGTAAAGGTTTACAGGAAATTATGACTATATCAAC 467
DB 531 AAAAAAAMAAAAAAGKAGAGGGRGBVAGRGDAATAAATAAAAAADTTKDWDA 590
QY 468 TAGACGCAAGCATGCTAGTAAAGATGATGACAATCGAGGCACTAGTAACGA 527
DB 591 GAAARAAAAADAARAAAKWTAAARAAAAAAGTTTAAATAAAAAAGG 650
QY 528 GTATGCAATGTTGATTAATTTTCGAAAAAGATATGCCAAATTCAGAGAAAGAACTT 587
DB 651 GAGCTGKGAADDDGAAADAVRRGRGRRAAARAAAAAADAARAAAAA 710
QY 588 TGAATTTTATTTGTTACCACTATATGCAAGCGCGCAATTTGCAATTAATTTATAG 647
DB 711 AAAADAGRRKWKGGKGGKATKTAAMAKGRKDWATATATMTWDTATWKAATD 770
QY 648 AGATGCGATATATTTGACAGACAGTGCAGCAATTAAGTGAAGAAATTCGATATATTA 707
DB 771 AKRAAAGRRRRDRARBDGRRARRRRRAAAGKARAGARRAR- - - -ARRAADR 825
QY 708 TATCAGACTCAAGACTGATTAGAGAAATTAAGATCATTTGATTAACATTTCTATACCA 767

DB 826 DWDMAAAAAAMAAAAAMTWPRDWWDDWDTWRDDDTTAAWMDARARRRRRRR 885
QY 768 GGGTTAAATTCATTTAATGCTCAATGCTCAAGATGGAGCTTTAATAGTTTCG 827
DB 886 RRRRRARRRRADDDTDTKDRWADATTDKDTTWTTTDDDDWAKARDRMAAKAGAMK 945
QY 828 TACAGATATGACATTAACAGTATTAAGTCTCGCAATATTAATTTCAAACTATGATCCAG 887
DB 946 WRDRADDWAAATKDDDGWKKWGGKRGKDKKKWDDKGTGKDDDDWDKTTRDMMW 1005
QY 888 TAGTATTCATTTGACGATAAAACGAAATGACTAGAGAAATTTATACAGATCCAGG 947
DB 1006 WMTRTTMDWWMDGRRGRWTRRRRGAWWRADWADBDTGKDTTADKDKRTDTTKRD 1065
QY 948 GTTACTGGGGGTATTAAGAAAGTGAAGTACGA 979
DB 1066 GDDWRKDKDKKRDKKDDTKKDATWDDDD 1097

RESULT 8
CNS00E07 1101 bp DNA linear GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC;
DEFINITION BACR29P01 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL069440 GI:4949583
VERSION GSS.
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazuhiro Oosawa and
Aaron Memmose in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
BcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp. the same strain used for the library
pl and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR29P01"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN
Query Match 2.5%; Score 50.8; DB 10; Length 1101;
Best Local Similarity 36.8%; Pred. No. 0.43;
Matches 119; Conservative 45; Mismatches 159; Indels 0; Gaps 0;
QY 529 TATGCAATGTTGATTAATTTTCGAAAAAGATATGCCAAATTCAGAGAAAGAACTT 588
DB 569 WATATAAAMAAATTTAATTTTAAATTAATTAAGWMAAAMAAAMWATAAMHT 628

QY	589	GAATTTTATGTTACCGATATATGCAACAAGCCGGAATTTGATTAATTTATTAAGA	648
Db	629	WTAAATTTATATMTTAAATTTTAAATATTAATTTATTAATTTAAATTTAAATTTAAW	688
QY	649	GATCGTGAATTTATTTTGAGCACAAGTGCCAAATGAGTGATGATGAATTCGTGATTAATTAAT	708
Db	689	TATTAATAAATTTAAATTTAAATAAATAATTTTAAATTAATAAATAAATTTTATTTTATTT	748
QY	709	ATCAGACATCAAGACATGATTTAGAGAAATATTAAGATCATTTGATTAACATTTCTATTAACAG	768
Db	749	AAATTAATTTAAATTTAAATTTAAATAAATTTTAAATTTAAATAAATAAATTTAAATTTAAATAA	808
QY	769	GGTTAAATCAATTTTAAATCGCTCAAAATGCTCAAGATGGTGAGCGTTAATAGTTTTCGT	828
Db	809	TWTATTAATTTAAATTAATATATATATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA	868
QY	829	ACAGATATGACATTTAACGATATT	851
Db	869	WTTAAATTAATGTTAATTAATTAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAW	891
RESULT 9			
AGS44460/c			
LOCUS	AGS44460	856 bp	DNA linear GSS 23-DEC-2004
DEFINITION	Mus musculus molossinus DNA, clone:MSMG01-458L01.T7, genomic survey		
ACCESSION	AGS44460		
VERSION	AGS44460.1		
KEYWORDS	GI:48304874		
SOURCE	GSS.		
ORGANISM	Mus musculus molossinus (Japanese wild mouse)		
REFERENCE	Mus musculus molossinus		
AUTHORS	1. Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriaki, K. and Shiroyoshi, T.		
TITLE	Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis		
JOURNAL	Genome Res. 14 (12), 2439-2447 (2004)		
PubMed	15574823		
REFERENCE	2 (bases 1 to 856)		
AUTHORS	Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-NOV-2003) Maehara Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-5031-9111, Fax: 81-45-5031-9170)		
COMMENT	Clones are derived from the mouse BAC library MSMG01. For BAC library availability, please contact Kunihya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp		
PRIMERS	Sequencing : T7		
LIBRARY	Vector : pBACe3.6		
R.Site 1	R.Site 1 : ECORI		
R.Site 2	R.Site 2 : ECORI.		
FEATURES	Location/Qualifiers		
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	/mol_type="genomic DNA"		
	/sub_species="molossinus"		
	/db_xref="taxon:57486"		
	/clone="MSMG01-458L01.T7"		
	/sex="male"		
	/tissue_type="mixture of kidney and spleen"		

ORIGIN	/clone_11b="MSMg01 Mouse Male BAC library"
Query Match	2.5%; Score 50.6; DB 10; Length 85c;
Best Local Similarity	47.8%; Pred. No. 0.46; Mismatches 153; Indels 0; Gaps 0;
Matches 140; Conservative	0;
OY	550 TTGCAAAAGATATATGCCTAATTTCAGAAAAGAACTTTGAATTTTTATGTACCAGTA 609
Dd	821 TTGGAAAAATGAGTGTGAAAAAAGTGTTGAGAAAGAGTGTTATATATATTTTTTAATA 762
OY	610 TATGCACAAGCCCGGAATTTGCATTTATATTTATTAAGAAGATGCTGATATTTTGAGACA 669
Dd	761 TTTTGTAAAAAAGTNGTGTATATAAATTTTGATATAATTTTAAAAATTAATAAAAA 702
OY	670 CAGTGGCAATTAGGTGATGATGAATTCGATATATATATCAGACTRCAAAGACTGATT 729
Dd	701 AATTNNATATATNTTTTAAATTTAAATTAATTTTAAATTAATAAAAAAATATATA 642
OY	730 AGAGATATATAAGTCATTCGATTAACATTCATTAACAGAGTTAAATCAATTTAATGCC 789
Dd	641 TATTTTATATAAATATATATATAAATATATATCATATAAATTAATAAAAAAATTTTA 582
OY	790 TCAATGCTCAAGATTGGTGAGCTTTAATAGTTTGTCACAGATATGACATT 842
Dd	581 AAAATTTTATAGAAATATATTTGTTATATATATATATATTAATTAATATATATTT 529
RESULT 10	
LOCUS	CG403581 707 bp DNA linear GSS 02-SEP-2003
DEFINITION	ZMMBB0248A07.r ZMMBB Zea mays genomic clone ZMMBB0248A07 3' ,
ACCESSION	CG403581
VERSION	CG403581.1 GI:34402465
KEYWORDS	GSS.
SOURCE	
ORGANISM	Zea mays
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea. Yu.Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J and Wing,R. Sequencing of the maize genome Unpublished (2003) Contact: Rod Wing Arizona Genomics Institute University of Arizona Biological Sciences West, 440A, P.O. Box 210088, Tucson, AZ 85721-0088, USA Tel.: 520 626 3967 Fax: 520 621 9288 Email: rwing@genome.arizona.edu PCR Primers FORWARD: T7 BACKWARD: M13r Plate: 0248 row: A column: 07 Seq primer: M13r Class: BAC ends.
FEATURES	location/Qualifiers
Source	1..707 /organism="Zea mays" /mol_type="genomic DNA" /cultivar="B73" /db_xref="taxon:4577" /clone="ZMMBB0248A07" /lab_host="DH1.0B" /clone_11b="ZMMBB0" /note="Vector: pBelOBAcl1; Site 1: HindIII; Site 2: HindIII; Zea mays L. sep. mays"
ORIGIN	

/db_xref="GDB:5378461"
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/clone="384M15"
/sex="Male"
/cell_type="Sperm"
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/note="Vector: pBelOAC11, Site_1: HindIII, Site_2: HindIII"

ORIGIN

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Best Local Similarity 46.3%; Pred. No. 0.95;
Matches 162; Conservative 0; Mismatches 188; Indels 0; Gaps 0;
QY 1047 TCTCTAACACCTGGCTTATCGTATTTTGTATATACAGAGCTAGATATATGTC 1106
DB 126 TTTATATATATATGATATATATATATATATATATATATATATATATATATAT 185
QY 1107 TGATGTAGAAATATTTGGGAGGCGATCATTAGTTGAAATGGAATGATGTTCTGA 1166
DB 186 TATTAATGTAT 245
QY 1167 AATTAACCATACCTTGGTAAACGATCTATATCTCCATCAATATTTTATTCG 1226
DB 246 TATATTTTATATATATATATATGTTTATATATATATATATATATATATATAT 305
QY 1227 GAACCTTTCGTTTGTAGTATGAGTCTGCTCGATATATTTTGAAGAACAGAGC 1286
DB 306 TAT 365
QY 1287 TATATAAT 1346
DB 366 TAT 425
QY 1347 AATTAATGACCTGATCTTAAAGATACGAAGTCCGCTCAATCTTCAT 1396
DB 426 ATATAATGTAT 475

RESULT 13
AJ925976 1110 bp mRNA linear EST 10-JUN-2005
LOCUS AJ925976 Theileria annulata merozoite Theileria annulata cDNA clone
DEFINITION cam009h03_g1k, mRNA sequence.
ACCESSION AJ925976
VERSION AJ925976
KEYWORDS EST.
SOURCE Theileria annulata
ORGANISM Theileria annulata
Bukaryoca; Alveolata; Apicomplexa; Picoplasmida; Theileridae;
Theileria.

REFERENCE 1 (bases 1 to 1110)
Pain,A., Renaud,H., Berriman,M., Murphy,L., Yeats,C.A., Weir,W.,
Kerhoulou,A., Aslett,M., Bishop,R., Boucquier,C., Cochet,M.,
Coulson,R.M.R., Cronin,A., de Villiers,E., Fraser,A., Foster,N.,
Gardner,M., Goble,A., Griffiths-Jones,S., Harris,D.E., Katzer,F.,
Laird,N., Lord,A., Maser,P., McKellar,S., Mooney,P., Morton,F.,
Nene,V., O'Neill,S., Price,C., Quail,M.A., Rabinowitsch,E.,
Rawlings,N.D., Rutter,S., Saunders,D., Seeger,K., Shah,F.,
Squares,R., Squares,S., Tivey,A., Walker,J.A., Woodard,J.,
Dobbelaeere,D.A.E., Langsley,G., Rajandream,M.-A., McKeever,D.,
Shiels,B., Tait,A., Bartell,B. and Hall,N.
TITLE The genome of the host-cell transforming parasite Theileria
annulata and a comparison with T. parva
JOURNAL Unpublished (2005)
COMMENT Contact: Pain A
The Pathogen Sequencing Unit
The Wellcome Trust Sanger Institute
Genome Camps, CB10 1SA, UNITED KINGDOM
Merzoite cDNA library: Frank Katzer and Brian Shiels, Division of
Veterinary Infection and Immunity, ICM, University of Glasgow, UK.
location/Qualifiers
1. .1110

FEATURES

source

/organism="Theileria annulata"
/mol_type="mRNA"
/isolate="Ankara (clone D7)"
/db_xref="taxon:5874"
/clone="cam009h03_g1k"
/dev_stage="merozoite"
/lab_host="Bos taurus (cow)"
/clone_1lb="Theileria annulata merozoite"
/note="country: Turkey; Ankara"

ORIGIN

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Best Local Similarity 29.8%; Pred. No. 1;
Matches 108; Conservative 0; Mismatches 254; Indels 0; Gaps 0;
QY 389 AAGATATAGATCAGCGTGTAAAGAAAATGCTTATAGAGCTAGAGGTTTACAGGAA 448
DB 710 AA 769
QY 449 TTATGAGACTATATCAAACTAGCTGCAAGCATGGCTATTAACAAGATGATGACAATC 508
DB 770 NTANANANANNNNNNAAAAATTAANANNNNTNANANANNNNANANANNNNTA 829
QY 509 GGAAGGCACTAGTAAGCGATGCAATGTTGATTAATCTTTCCAAAAGAAATATGCCA 568
DB 830 NNNNNNTTTNNNANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAA 889
QY 569 AATTCAGGAAAGAACTTTGAAATTTTGTGTTACAGATATGCAAGCCGCAATT 628
DB 890 NNNANNNNTTANNNNNNTNNNTTNTTNTTNTTNTATATATATATATATATATAT 949
QY 629 TGCATTTAATTTTATTAAGATGCTGATTTTGGAGACAGCGCAATTAGTGATG 688
DB 950 TATTAAGTTATTTTAAATATATATTAANAAAAATTAATATATNTTNTTATATATA 1009
QY 689 ATGAATTTGCTGATATTTATATCAGCTACAGACTGATTAGAAATTAAGATCAT 748
DB 1010 NNNAAATTAATGNNAAAAATATNTAATTAATTAATTTATAGATTAATTAATTA 1069
QY 749 GT 750
DB 1070 NT 1071

RESULT 14
CNS02HA4 989 bp DNA linear GSS 01-SEP-2000
LOCUS CNS02HA4 Tetradon nigroviridis genome survey sequence T7 end of clone
DEFINITION 139021 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION AL197365
VERSION AL197365
KEYWORDS GSS; genome survey sequence.
SOURCE Tetradon nigroviridis
ORGANISM Tetradon nigroviridis
Bukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetradon.

REFERENCE 1
Roest Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quelier,F.,
Saurin,W. and Weissenbach,J.
TITLE Estimate of human gene number provided by genome-wide analysis
using Tetradon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
PUBMED 10835645

REFERENCE 2
Roest Crolius,H., Jallion,O., Dasilva,C., Ozouf-Coataz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quelier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis

JOURNAL Genome Res. 10 (7), 939-949 (2000)
PUBMED 10899143
REFERENCE 3 (bases 1 to 989)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

FEATURES
source
1. .989
/organism="Tetraodon nigroviridis"
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/db_xref="taxon:99883"
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end : T7"

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Matches 169; Conservative 5; Mismatches 205; Indels 0; Gaps 0;

QY 975 TAGAGTACCTCCGTTGATATATCTATATATACACCTTACGCTATGGAATAATACGC 1034
DB 62 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 121
QY 1035 AAGACGACGCTCTTCTTATACCACTTGGCTTAATCGATTTTGTATATACAGACTCT 1094
DB 122 AAAAACTAC 101
QY 1095 AGGTATATGCTCGATGTGAGAAATTTGGGAGGACATCACTTAAGTGAATAATGAAA 1154
DB 182 TACTAATACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 241
QY 1155 TGATGGTTCGAATATACCACTTGGTAAACGATTTCTATTCTCTATTCATA 1214
DB 242 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 301
QY 1215 TTTTAATTTGCGAACCCTTCTGTTTCAATTTGAGTCACTTCTGTTATATTTAGG 1274
DB 302 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTGC 361
QY 1275 AGGAACAGAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTAA 1334
DB 362 TAATACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 421
QY 1335 TACATCAATATATATATAT 1353
DB 422 TACTACTAATATATATATAT 440

RESULT 15
CZ239945 886 bp DNA linear GSS 11-FEB-2005
LOCUS A1AA-aat46907.b1 Ancylostoma caninum whole genome shotgun library
DEFINITION (A1AGSS 001) Ancylostoma caninum genomic, genomic survey sequence.
ACCESSION CZ239945
VERSION CZ239945.1 GI:59625386
KEYWORDS GSS.
SOURCE Ancylostoma caninum (dog hookworm)
ORGANISM Ancylostoma caninum
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidae; Ancylostomidae; Ancylostomatinae; Ancylostoma.
REFERENCE 1 (bases 1 to 886)
AUTHORS Mitrava, M., McCarter, J.P., Pape, D., Ritter, E., Tsagaris, H., R.,
Ronko, I., Martin, D., Wylie, T., Dante, M., Meyer, R., Messina, D.,
Waterston, R.H., Clifton, S.W. and Wilson, R.
TITLE Genome Survey sequences from the parasitic nematode Ancylostoma

JOURNAL caninum
PUBMED Unpublished (2004)
REFERENCE Contact: Mitrava M
AUTHORS Washington University in St. Louis
TITLE Washington University School of Medicine
JOURNAL 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
COMMENT Genomic DNA provided by John Hawdon (mcmj@wumc.edu) DNA
sequenced by Washington University Genome Sequencing Center
Class: Shotgun.

FEATURES
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1. .886
/organism="Ancylostoma caninum"
/mol_type="genomic DNA"
/strain="Baltimore"
/db_xref="taxon:29170"
/dev_stage="Adult"
/lab_host="GS10"
/clone_1lb="Ancylostoma caninum whole genome shotgun
library (A1AGSS 001)"
/note="Vector: pOTW13; Site 1: BstXI; Site 2: BstXI;
Ancylostoma caninum genomic DNA was randomly sheared,
end-repaired and size fractionated to enrich for 2-4 kb
fragments. Genomic DNA was provided by John Hawdon
(mcmj@wumc.edu) at George Washington University.
Sequencing by Washington University Genome Sequencing
Center, St. Louis, MO."

ORIGIN
Query Match 2.4%; Score 48.4; DB 10; Length 886;
Best Local Similarity 45.3%; Pred. No. 1.6;
Matches 175; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

QY 992 ATATCTTAATATATACACCTTACTGCTATGGAATAATACGACGCTCTTCTT 1051
DB 417 AT 358
QY 1052 ATACCACTTGGCTTAATCGATTTTGTATATACAGACTCTAGTAAATATGTCGATG 1111
DB 357 AT 298
QY 1112 TGAGAAATATTTGGGAGGACATACATTAAGTGAATGGAATGATGTTCTGAATAA 1171
DB 297 AT 238
QY 1172 CCCATACCTTGGTAAACGATTCCTATTAATTTTAAATTTTGGCAACC 1231
DB 237 AT 178
QY 1232 TTTCTGTTTCAATTTGAGTCACTTCTGTTATATTTGAGGAGACAGGCTTAATA 1291
DB 177 AT 118
QY 1292 AT 1351
DB 117 GTAT 58
QY 1352 ATGTACTGATCTTTTAT 58
DB 57 AT 32

Search completed: December 24, 2005, 18:48:57
Job time : 7459 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 13:22:10 ; Search time 391 Seconds

(without alignments)
9315.150 Million cell updates/sec

Title: US-10-782-096-1

Sequence: 1 atgattcattatcaataaataa.....atgattcattatcaatcaa 2049

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/1 COMB.seq: *
2: /cgn2_6/prodata/1/ina/5 COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	256.2	12.5	3471	2	US-07-876-280-29
2	256.2	12.5	3471	2	US-07-812-180A-1
3	256.2	12.5	3471	2	US-08-315-468-1
4	256.2	12.5	3471	3	US-07-941-650A-1
5	236	11.5	3504	3	US-10-089-678-2
6	236	11.5	3690	3	US-10-089-678-3
7	235.6	11.5	3507	2	US-08-315-468-3
8	231	11.3	1607	3	US-08-286-870A-5
9	231	11.3	1946	3	US-08-286-870A-3
10	229.4	11.2	2965	2	US-08-460-570-1
11	229.4	11.2	2965	2	US-08-460-570-2
12	229.4	11.2	2965	3	US-08-286-870A-1
13	229.4	11.2	2965	3	US-08-286-870A-2
14	223.6	10.9	3684	2	US-08-448-170-7
15	223.6	10.9	3684	3	US-08-961-803-5
16	223.6	10.9	3684	3	US-09-661-322A-62
17	220	10.7	2133	3	US-09-661-322A-41
18	216.4	10.6	3797	2	US-07-915-203-1
19	216.4	10.6	3797	2	US-08-272-887-1
20	216.4	10.6	3797	2	US-08-789-449-1
21	209.6	10.2	4074	3	US-08-377-690-1
22	207.8	10.1	3471	3	US-09-002-285-73
23	207.8	10.1	3471	3	US-09-589-477-73
24	207.8	10.1	3471	3	US-09-661-322A-27

25	207.8	10.1	3471	3	US-10-099-285A-73	Sequence 73, Appl
26	207.8	10.1	4344	2	US-08-532-547-4	Sequence 4, Appl
27	207.8	10.1	4344	2	US-08-379-656B-4	Sequence 4, Appl
28	207.8	10.1	4344	3	US-08-455-838-4	Sequence 4, Appl
29	207.8	10.1	4344	3	US-09-019-809-4	Sequence 4, Appl
30	207.8	10.1	4344	3	US-09-471-177-4	Sequence 4, Appl
31	207.8	10.1	4344	3	US-09-220-806-4	Sequence 4, Appl
32	206.8	10.1	1561	2	US-08-532-547-2	Sequence 2, Appl
33	206.8	10.1	1561	2	US-08-379-656B-2	Sequence 2, Appl
34	206.8	10.1	1561	3	US-08-455-838-2	Sequence 2, Appl
35	206.8	10.1	1561	3	US-09-019-809-2	Sequence 2, Appl
36	206.8	10.1	1561	3	US-09-471-177-2	Sequence 2, Appl
37	206.8	10.1	1561	3	US-09-220-806-2	Sequence 2, Appl
38	204.6	10.0	4173	3	US-09-661-322A-37	Sequence 37, Appl
39	204.4	10.0	3414	2	US-07-973-320-3	Sequence 3, Appl
40	204	10.0	2180	2	US-09-003-217-1	Sequence 1, Appl
41	203.2	9.9	1464	2	US-08-448-170-9	Sequence 9, Appl
42	203.2	9.9	1464	3	US-08-961-803-6	Sequence 6, Appl
43	201.2	9.8	3414	2	US-07-973-320-1	Sequence 1, Appl
44	201	9.8	1629	6	PCT-US91-02560-3	Sequence 3, Appl
45	200.8	9.8	1897	3	US-09-363-970-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-07-876-280-29
Sequence 29, Application US/07876280
Patent No. 5262158
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
APPLICANT: Cannon, Raymond J.C.
TITLE OF INVENTION: No. 5262158 Bacillus thuringiensis Isolates for
NUMBER OF SEQUENCES: 30
TITLE OF INVENTION: Controlling Acarides
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,280
FILING DATE: 19920430
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S 104
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C

;
; IMMEDIATE SOURCE:
; CLONE: E. coli NM522 (pMYC2320) NRRL B-18769
; US-07-876-280-29

Query Match	12.5%	Score 256.2;	DB 2;	Length 3471;
Best Local Similarity	50.5%;	Pred. No. 9.5e-53;		
Matches 838;	Conservative 0;	Mismatches 778;	Indels 45;	Gaps 7;

Qy	13	AAAAATAAAATGAATAGAAATGTTGATGCTTTACAAATCACTCAATATGCTAAT	72
Db	10	AATATATCAAAATGAAATATGAAATTTAGATGAGACCTTCAATC---TGATTCAGT	66
Qy	73	TGTTATCCAAAGTATCCACTAGCAAAAGATCCAAATGACTATGCGAACAAGCAAT	132
Db	67	GATTTCAACAGATATCCCTTTTGCGAATGAGCCAAAGATGCGTTCAAAAATATGAAATAT	126
Qy	133	AAAGAATGCTAAATATATGTTGATTCAAAATACAAATTTATTTGGATATATAGACGTA	192
Db	127	AAAGATTATTCGAAAATGCTGGG-----GGAGAGATTCGTAATTA	168
Qy	193	TCTAGCCCTGAAGCTCTTTAAAGTACGAGATGCTGTTTTAAACGGTATTAACAGTGA	252
Db	169	TTTGGAATATCCGGAGACGTTTATTAAGTTATCCACAGATTTCAAACTGGAATTGCAATGTT	228
Qy	253	GGGACTATACTTTGCAATTTAAGGGTCCCTTTGGCAAGTCAATCATTTGGAATTAATAGT	312
Db	229	GGTGAATACTAGAGGCTTTAGGGGTTCCATTTGCTATCAGATATGATGTTCTATAGT	288
Qy	313	AGGCTAATAGGTAATTTTATTTGGGCGA-----GGCCTGATCCATTTGAAGCACTTAATGTT	366
Db	289	TTCAATGTTGGTCAATTAATGCGCTCAAAAGCGTAGATATATGGGGAAATTAATGAA	348
Qy	367	CTTGTGGAAGCTTAATTAAGAAAATGATAGATCAAGCTGTATAGAAAATGCTCTTAGA	426
Db	349	CGATGGAAGAACTCGCTTGATCAAAAATATGTAAGAAAATATGTAAGAGATTAAGCTCTTGCT	408
Qy	427	GAGCTAAGAGTTTACAGGAAATTAATGACTATATCAACTGACCTGCAAGCATGCGTA	486
Db	409	GAATTTAAAGGGCTAGAGAAATGCTTTGGATGATATATCAGCAGTCACTTGAAGATTTGGCTG	468
Qy	487	GTTAACAAAGATGATG---ACAACTGGAGGGGCACTAGTAAGGCAATATGCAATGTTGAT	543
Db	469	GAATAATGCGAATGATGCAAGAACTTGAAGTGTGTTCTTAATCAATTAATAGCTTAAGT	528
Qy	544	AACTTTTTCGAAAAGATATGSCAAAATTCGAAGAAAGAACTTTGAATTTTATGTTA	603
Db	529	CTTAACCTTTGTTATGTTCAATTCACATCTTTGAGATACCGGACAGAGTACTATATTA	588
Qy	604	CCAGTATATGCAACAAGCCCGCAATTTGCATTAATTTATTTATTAAGATGCTGATATTTT	663
Db	589	GCAGTATATGCAACAGGCTGTGAACCTCAATTTATGTTATTAAGATGCTCTTCTATTTTTT	648
Qy	664	GGACCAAGTGGCAATTAAGTGAATGATGAATAATTCGTGATTAATATATGCACTACAAGA	723
Db	649	GGAGAGAGTGGGGATTTACACACAGGTAAATTTCTAGATTTTATTAATCGTCAATGCAA	708
Qy	724	CTGATTAGAGATATTAAGATCATTTGTAATCACTTCTAATTAACAGGGTTTAAATCAATTT	783
Db	709	CTTACCGCTGAATATTCAGACATATTTGTGTAAGTGTATTAATATGGGCTTAGATAAATTG	768
Qy	784	AATGCTCAATGCTCAAGATTTGGGTAGCTTTAATAGTTTTCGTACAGATATGCAATTA	843
Db	769	AAAGGTACCACTTCTAATAAGTTGGCTGAATTAATCATCGATTCCTGGTAGAGATGCAATTA	828
Qy	844	ACAGTATTAAGATCTCGCAATTAATTAATTCCAACATATGATCCACGTAAGGATATCCATTACA	903
Db	829	CTGGTATTAATGATTTGGTGGCGTTATTTCCAACTATGACACACATATGATATCCAAATCGAA	888
Qy	904	GTAATAAAACGATTTGACTAGGAAATTTATACAGATCCAGTATAGGGTTTTACTGGGGTATTA	963
Db	889	ACAACAGCTCACTTACACGGGAATGTATATACAGATCCGATATGCAATTTATACATATGTACA	948
Qy	964	GAATGTGAGGTAGGACTTACCTTTGGTATATCTAATTAATACACCTTTATCTGCTATG	1023

Db	949	AGTACTGGATTCTGCA---ACCCCTGGTCAACCCACAGTGGTATCTCTTTTATGAAGTT	1005
QY	1024	GAAATTAAGCAGACGAGCGTCCCTTCTTAATCACTTGGCTTAATGCTATTTTGTATAT	1083
Db	1006	GAAATCAACGTAAATCTCCCGCACACCTTGTGGATATATCTACGCTCAGTAAATTAAT	1065
QY	1084	ACAAGACCTCAGGTAAATATGT-----CTGATGTGAATAATTTTGGGAGGCGAT	1134
Db	1066	ACAATGTAGAGGGGTATTACGTTAAATATATGATGATATATTAATCTAGTCAAGACAT	1125
QY	1135	ACATTAGTTGAAATGAAATGTATGTTCTGAAATACCCATTAACCTTGGTAAACGTAT	1194
Db	1126	ACCCATAAATATGTGTAACAGCTGATTCGACGGTAAATACACAGCTATATTACGGTGA	1185
QY	1195	TCTATTACTCCTATTCATAATTTTAATTTCGCAACCTTTCGTTTTCAGTATTAGTCA	1254
Db	1186	ATCATCTTCAGAAAAGAAATTCATTGTGCACTTGAGAGATAGGATATTTTGAATTAATTC	1245
QY	1255	CTTGCTCGTATATATTTAGAGGAAACAGAGCGTAATTAATATATTACTATCAGTATGA	1314
Db	1246	ACTGTGSCAA--ACCTAGCTAATTACTACCAAAAGGCATATGGTGTGCCGGATCTTGG	1302
QY	1315	GTCCTGAGAGTTATTTTAAATATACATCAAAATATTAATATGATACCTGGATCTTTAAGTAC	1374
Db	1303	TTCCATATGTGTTAAAGGGGAACCTATCAACAACAGCGATTATTAATTAATAAACAT	1362
QY	1375	GAAGTGCCTGCTAATCTTCCATCCCAACTATATATTACAGAAATTAACAGAAAGATTAAG	1434
Db	1363	ACAGCTCTCCAAAGGGGTGACAGAGTTTATGAATCAAGTATGAATAATCCTCTAGATAGA	1422
QY	1435	CCAAAGCAAAACCGAGAGATTTACGCAATAGATTTATCTATATATCAAAATTTTGTAGCA	1494
Db	1423	ACGTGTACCGGTAGCTGAAGCTATAGCTATAGATATATCTATATATACCTCCCATTTCTTC	1482
QY	1495	CGGCGAAGTAGTTACAGCGGCTATTTGTATGTCCTTTAAAGTTTGGTGGGACATACCAAT	1554
Db	1483	TCTAAAAATGGAGGTGATATCTATGGAGTTTCCCTGTATTTGTGTGGAACATATCTAGT	1542
QY	1555	ATGAGATGTATATATGCTCTTGAAACAGATAAATTAATCTCAAAATGATGCAAGTTAAAGGT	1614
Db	1543	GCGGATTTAAATATATCAATATATTTCAGATAAATATCACTCAAAATTCACGCGGTAAAGGA	1602
QY	1615	TGGGGGGGGAATATCGGGTTTGTATCCCGAGACATATGCG	1655
Db	1603	GACATGTTATATCTAGGGGGTTCCTGATGACAGGTCCTGCG	1643

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1 RESULT 2
2 US-07-812-180A-1
3 Sequence 1, Application US/07812180A
4 Patent No. 5366892
5
6 GENERAL INFORMATION:
7
8 APPLICANT: Foncecrada, Luis R
9
10 APPLICANT: Payne, Jewel M
11
12 APPLICANT: Sick, August J
13
14 TITLE OF INVENTION: No. 5366892e1 Coleopteran-Active Bacillus
15 TITLE OF INVENTION: Churingiensis Isolate and a No. 5366892e1
16 TITLE OF INVENTION: Coleopteran-Active Toxin
17
18 NUMBER OF SEQUENCES: 2
19
20 CORRESPONDENCE ADDRESS:
21
22 ADDRESSEE: Roman Saliwanchik
23 STREET: 2421 N.W. 41st Street, Ste A-1
24
25 CITY: Gainesville
26
27 STATE: FL
28
29 COUNTRY: USA
30
31 ZIP: 32606
32
33 COMPUTER READABLE FORM:
34
35 MEDIUM TYPE: Floppy disk
36
37 COMPUTER: IBM PC compatible
38
39 OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
40
41 SOFTWARE: Patentin Release #1.0, Version #1.25
42
43 CURRENT APPLICATION DATA:

```


APPLICATION NUMBER: US/07/812,180A
FILING DATE: 19920102
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sallimanchik, Roman
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C
IMMEDIATE SOURCE:
LIBRARY: LAMBDAEM (TM) - 11 LIBRARY OF LUIS
CLONE: 50C
US-07-812-180A-1

Query Match 12.54; Score 256.2; DB 2; Length 3471;

Best Local Similarity 50.54; Pred. No. 9.5e-53; Matches 838; Conservative 0; Mismatches 778; Indels 45; Gaps 7;

13 AAAAAATGAATGAATGAATGTTGATGCTTACGAATCAACTTAATATGCTAAT 72
10 AATATATCAATATGATATGAAATTTATAGATCCAGACCTTCTACATC---TGATCCAGT 66
73 TGTATTCAGAGTATCCACTAGCAAAAGATCCAAATGACTATGCGAAACAGCACTAT 132
67 GATTCTACAGATACCTTTTGCGAATGAGCCAAAGATCGTTACAAATATGAATTAAT 126
133 AAGGAATGGTAATATGATGATCAAAATACAAATTTATGCTATATAGACACTAT 192
127 AAGGATTATCTGAAATGCTCGG-----GGAGGAATCTCGAATTA 168
193 TCTAGCCCTGAAGCTGCTTAAGTATCGAGATGCTTTTAAAGGATATTAACAGTGA 252
169 TTTGGAATCCGAGAGCTTTATAGTTCATCCAGATTCAAATGGAATTTGGCATTTG 228
253 GGAATATATCTTGAATTTAGGGGTCCTTTGGCAATCAATCATTTGGAATTAATAGT 312
229 GGTGATATATAGAGAGCTTTAGGGGTCATTTGCTAGTCAGATAGCTTCTATAGT 288
313 AGGCTATATAGTATTTTATGGGAG-----GGCTGATCATTTTGAAGCATTTAGGTT 366
289 TTGATTTGTTGCTCAATTTATGCGCTCAAAAGGCTATATATATGAGGAAATTAAGGA 348
367 CTGTTGAAGAGCTTATTAAGAAAGTATAGTACGCTGTAAGAGAAATGCTCTAGA 426
349 CGATGAGAAATCTGTTGATCAAAAATATGAAATATATATATATATATATATATATAT 408
427 GAGCTAGAAAGCTTACAGGAATTTATGAGACTATATCAAACTAGACTGACAGAGCTGA 486
409 GAATTAAGAGGCTAGGAATATGCTTTGATATATATAGCAATCACTTGAAGATGGCTG 468
487 GTTAAACAGAAATGAT---ACATCGAGGGCACTAGTAAACGATATGCAATTTGTTGAT 543
469 GAAATTCGCAATATATGCAAGAACTAGAAAGTGTGTTCTATCAATTAATATAGCTTAGAT 528
544 AACTTTTGAAGAAATATGCAAAATTCAGGAAAGAAACTTTGAATTTTATTTATTTGTTA 603
529 CTTAACCTTTTGTGTTCAATTTCCATCTTTTGCAGTATCCGAGACGAAATGATATTTA 588
604 CCAGTATATGACAAAGCCGGAATTTGCAATTTATTTATTAAGAGATGCTGATATTTT 663

589 GCAGTATATGACAGAGCTGTGAACCTTACATTTATTTATTAAGATGCTTCTATTTT 648
664 GAGCAGAGTGGCAATATAGGTATGATGAATTCGTATATATATATATATATATATATAT 723
649 GAGAAAGTGGGATTTTACACAGGTGAATTTCTGATTTATATATATATATATATATATAT 708
724 CTGATTAAGATATTAAGATCATTTGATATACATTTATTAACAGGCTTTAATCAATTT 783
709 CTTAACCGCTGAATATATGAGACTATTTGTTAAAGGTATTAATAATCGCTTATGAATTTG 768
784 AATGCTCAATGCTCAAGATTTGGTGAAGCTTTAATAGTTTGTATACAGATATGACATTA 843
769 AAGGTACCACTTCTAAAGTGTGTAATATATATATATATATATATATATATATATATAT 828
844 ACAGTATATATATCTGCAATATATATTTCCAACTATGATCCAGTATGATATATATATAT 903
829 CTGATATTAATTTGGTGGCTTATTTCCAACTATGATCCAGTATGATATATATATATAT 888
904 GTAAAAACGAAATTTGATGAGAAATTTATATACAGATCCAGTATGATGATGATGATGAT 963
889 ACAACAGCTCACTTACACGAGATGTATATACAGATCCAGTATGATATATATATATATAT 948
964 GAAAGTGAAGTATGAGACTTACCTGCTGATATATCTTATATATATATATATATATATAT 1023
949 AGTACTGATTTCTGCA---ACCTTGTGCAACCCAGAGTGTATCTTTTATTAAGATT 1005
1024 GAAATATACGCAAGACAGCTCTTCTTATATACACTTGGCTTATATGATTTTGTATAT 1083
1006 GAAATACAGCTAATTTGCTCCGACACTTGTGATATATCTAGCTAGATGAATTAAT 1065
1084 ACAAGACTCTAGATATATATGCT-----CTGATGAGAAATATATTTGGAGGAGCAT 1134
1066 ACAAGTGAAGGGGATTTATGATTAATATATATATATATATATATATATATATATATAT 1125
1135 ACATTAATGAATATGAATATGATGCTTCTGAATATATCCATATATATATATATATATAT 1194
1126 ACCCTAATATATGATGAAACAGCTGATTCAGCCGTATATATATATATATATATATAT 1185
1195 TCTATTAATCTCTATTCATATTTTAAATTTGCGCAACCTTTCTGTTTCAATGATGATCA 1254
1186 ATCACTTCAAGAAAGATATATATTTGCACTTGAGATATGAGATATTTTGAATATATATCA 1245
1255 CTGCTGCTATATATTTAGAGGAAACAGAGCTAATATATATATATATATATATATATAT 1314
1246 ACTGTGGCA---ACCTAGCTAATATATCAAAAGCATATATGATGCGGATCTTTG 1302
1315 GTCTCGAGATATTTTAAAT 1374
1303 TTCCATATGTTAAAGAGGCACTCATCAACAGCTATATATATATATATATATATATATAT 1362
1375 GAGTGTCTGCTATATCTTCCATCCAACTATATATATATATATATATATATATATATAT 1434
1363 ACAGCTCTCCAGAGGTATATACAGTTTATGAATCAAGTATGAATATCTTATAGATGA 1422
1435 CCAAGCAAAACCGAGAGATTTCAAGCATATATATATATATATATATATATATATATATAT 1494
1423 ACTGTACCGGTACTGAAAGCTATATGCTATATATATATATATATATATATATATATATAT 1482
1495 CGGCGAAGTATTTCAAGCGGTATTTGATCTTTTAAAGTTTGGTGGCAATATCAAGT 1554
1483 TCTTAAATATGAGAGTCACTATATGGAAGTTTCCCTGATTTTGGAGACATATATATAT 1542
1555 ATGATCTGATATATATGCTCTTGAACAGATATATATATATATATATATATATATATATAT 1614
1543 GCGATTTTAAATATATCAAT 1602
1615 TGGGGGGGGAATATCGGTTTGTATCCAGACTACTACTG 1655
1603 GACATATATATCTAGGGGTTCCGTATATATATATATATATATATATATATATATATAT 1643

RESULT 3
US-08-315-468-1

```

1 Sequence 1 Application US/08315468
2 Patent No. 5554534
3 GENERAL INFORMATION:
4 APPLICANT: Michaels, Tracy Ellie
5 APPLICANT: Foncecrada, Luis
6 APPLICANT: Narva, Kenneth E.
7 TITLE OF INVENTION: Process for Controlling Scarab Pests
8 TITLE OF INVENTION: with Bacillus thuringiensis Isolates
9 NUMBER OF SEQUENCES: 6
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: David R. Saliwanchik
12 STREET: 2421 N.W. 41st Street, Suite A-1
13 CITY: Gainesville
14 STATE: FL
15 COUNTRY: USA
16 ZIP: 32606
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: Patentln Release #1.0, Version #1.25
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/315,468
24 FILING DATE:
25 CLASSIFICATION: 424
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US/08/014,941
28 FILING DATE: 01 FEB 1993
29 APPLICATION NUMBER: 07/828,430
30 FILING DATE: 30-JAN-1992
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: 07/808,316
33 FILING DATE: 16-DEC-1991
34 ATTORNEY/AGENT INFORMATION:
35 NAME: Saliwanchik, David R.
36 REGISTRATION NUMBER: 31,794
37 REFERENCE/DOCKET NUMBER: MA73.C2
38 TELECOMMUNICATION INFORMATION:
39 TELEPHONE: 904-375-8100
40 TELEFAX: 904-372-5800
41 INFORMATION FOR SEQ ID NO: 1:
42 SEQUENCE CHARACTERISTICS:
43 LENGTH: 3471 base pairs
44 TYPE: nucleic acid
45 STRANDEDNESS: double
46 TOPOLOGY: linear
47 MOLECULE TYPE: DNA (genomic)
48 HYPOTHEICAL: NO
49 ANTI-SENSE: NO
50 ORIGINAL SOURCE:
51 ORGANISM: Bacillus thuringiensis
52 STRAIN: kumamotoensis
53 INDIVIDUAL ISOLATE: PS50C
54 IMMEDIATE SOURCE:
55 LIBRARY: LAMBDAEM (TM) - 11 LIBRARY OF LUIS
56 LIBRARY: FONCERRADA
57 CLONE: 50C(a)
58 /
59 us-08-315-468-1
60
61 Query Match 12.5%; Score 256.2; DB 2; Length 3471;
62 Best Local Similarity 50.5%; Pred.No.9,5e-53;
63 Matches 838; Conservative 0; Mismatches 778; Indels 45; Gaps 7
64
65 13 AAAATAAAATGAATATGAATGTTGGATGCTTTACAAATCAACTTAATATGCTTAAT 72
66 10 AATATATCAAAATGATATGAAATTTATAGATGACACCTCTTACATC---TGTATCCAGT 66
67 73 TGTATTCACAGATATTCACATAAGCAAAAGATCCACAAATGACTATGCGAAACAGCACTAT 132
68 67 GATTCTACACAGATACCTTTTGGCAATGAGCCAAACAGATGCGTTACAAAATATGATTAAT 126
69 133 AAAAGATGGCTAAATATATGTGTGATTCAAAATACACAATTTATTTGTGTATATAGACGGTAT 192
70

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Db	127	AAAGATTATCGAAAAGATGCTGGG-----GGAGGAAATCCGTAATTA	168
Oy	193	TCTAGCCCTGAAGTCGTTAAAGTATCGAGAGTCGTTTAAACGGGTATTAACAGTGA	252
Db	169	TTTGGAAATCCGGAGAGGTTTATTAAGTTCATCCACGATTCMAACTGGAAATGGCATGTT	228
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Db	229	GGTGAATTACTAGGAGCTTTTAGGGGTTCATTTGGTCTAGTCAAGTAAAGTAACTTCTAATGT	288
Oy	313	AGGCTAAATAGGATTTTATGGGAG-----GGCTGATCCATTTGAAGCATTTATGTT	366
Db	289	TTCAATGTGGTCAATTAATGAGCCGCTCAAGAGGCTAGATATTAAGGGAGAAATTAATGAA	348
Oy	367	CTTGTGAAGAGCTTATTAAGAAAAGTATGATCAGGCTGTAAAGAAAATGCTCTTAGA	426
Db	349	CGAGTGAAGAACTCGTGTATCAAAAATATGAAAATATGTAAAGATTAAGGCTCTTGCT	408
Oy	427	GAGCTAAGGTTTACAGGGAATTATGAGCTATATCAACTAGATCGCAAGCATGGCTTA	486
Db	409	GAATTTAAAGGCTAGGAAATGCTTTGATGTATATACAGATCATCTTGAAGATGGCTG	468
Oy	487	GTTTAAACAAGATGATG---ACAAATCGAGGGCATAGTAAACGAGTATGCAATTTGTAT	543
Db	469	GAATATGCAATGATGCAAGACTAGAAAGTGTGTTCTATCAATTAATATAGCTTATAGT	528
Oy	544	AACTTTTTCGAAAAGAAATATGCCAAATTCAGAGAAAACCTTGAATTTTATTTGTTA	603
Db	529	CTTAACCTTGTATGTTCAATTCATCTTTTGCAGTATCCGGAACGAAAGTATATTAATTA	588
Oy	604	CCAGTATATGCAACAAGCCGGAATTTGATCATTTATTTAATGAAGATGCTGATTAATTT	663
Db	589	GCAGTATATGCAAGGCTGTGAACCTATTAATTTGTTATTTAAGAGATGCTTCTATTTTT	648
Oy	664	GGAGCACAGTGGCAATTAAGTATGATGAATTCGTGATATTAATATCAACTACAGGA	723
Db	649	GGAGAAGTGGGATTTTACCAAGGTGAATTTCTGATTTTATTAATTCGCAAGTCCAA	708
Oy	724	CTGATTTAGAGATTAAGATCATTTGTATTAACATCTTAATAACAGGGTTTAAATCAATTT	783
Db	709	CTTACCGCTGAATTTGACACTATTTGTGTAAAGGTATTAATATCGGCTTAAGATAAATGTG	768
Oy	784	AATGCTCAATGCTCAAGATTTGGGTAGGCTTTAATAGTTTCTGATCAGATATGACATTA	843
Db	769	AAAGGTACACTTTTAAAGTTGGCTAATTAATATCATGTTCCGTAAAGATATACATTA	828
Oy	844	ACAGTATTAAGTCTCGCAATTAATTTCCAAACTATGATCCACGTAGATTCATTAACA	903
Db	829	CTGTATTAAGATTTGGTGGGCTTAATTTCCAAACTATGACACACTATGATTCCAATGAA	888
Oy	904	GTAAAAACGGAATTAAGTGAAGGATTTATACAGATTCAGTAGGGTTTATCTGGGGTATTA	963
Db	889	ACAACAGTCAACTTACACGGGATGTGTATACATCCGATAGCATTTAATCATATGTACA	948
Oy	964	GAAATGGAGGTAGAGCTTACCTTGGTATATCTATATAATCAACCTTTACTGCTATG	1023
Db	949	AGTACTGGATTTGCA---ACCTTGGTCAACCCACGTGTATTTCTTTTATGAAGTT	1005
Oy	1024	GAATATACGCAAGACAGCTCTTCTTAATACACTTGGCTTAATCGTATTTTGTATAT	1083
Db	1006	GAATTAACAAGTAATTCGTCCGCCACACTGTTGTATATCTCAGCTCAGTAAATTAAT	1065
Oy	1084	ACAAGACTAGTAATATATGT-----CTGATGTAGAAATATTTGGGGAGGGCAT	1134
Db	1066	ACAAGTGAAGGGGTATTAAGCTTAATATATGATGCATATATTAACCTAGTGTGAGCAAT	1125
Oy	1135	ACATTAGTGAATATGAAATGATGTTTGAATTAACCCATTACTTTGGTAAACGAT	1194
Db	1126	ACCCTAATATTCGTAGAACAGCTGATTTCCACGTTACATACACAGCTAATTAAGGTGCA	1185
Oy	1195	TCATATATCTCATATCAATTTTAATTTTCGCAACCTTTCTGTTTTCAGTATTAAGTCA	1254
Db	1186	ATCATCTCAGAAAAGATTAATTTGCACTTGAGATAGGAGATATTTTGAATTAATTAATCA	1245

|||||
Db 829 CTGATATTAGTATGAGCGTTATTTCCAACTATACACACGTACGTATCCATGAA 888
Qy 904 GTAAAAACGAAATTAGTAGGAAAGTTATATACAGATCCAGAGGCTTACGGGGTATTA 963
Db 889 ACAACGGCCCACTTACACGGAAAGTGTATACAGATCCAAATTAATTAACAGAAACA 948
Qy 964 GAAAGTGAGTAGGA 979
Db 949 AGTGATGATTTTGT 964

RESULT 6
US-10-089-678-3

/ Sequence 3, Application US/10089678
/ Patent No. 6962977
/ GENERAL INFORMATION:
/ APPLICANT: ASANO, Shinichiro
/ TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
/ FILE REFERENCE: 068821
/ CURRENT APPLICATION NUMBER: US/10/089, 678
/ PRIOR FILING DATE: 2002-04-03
/ PRIOR APPLICATION NUMBER: JP 2000-236140
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: PCT/JP01/06660
/ PRIOR FILING DATE: 2001-08-02
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 3
/ LENGTH: 3690
/ TYPE: DNA
/ ORGANISM: Bacillus thuringiensis
US-10-089-678-3

Query Match 11.5%; Score 236; DB 3; Length 3690;
Best Local Similarity 55.9%; Pred. No. 8,4e-48;
Matches 546; Conservative 0; Mismatches 400; Indels 30; Gaps 4;

Qy 13 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 72
Db 196 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 252
Qy 73 TGTATTCAGAGTATCCATAGCAAGAAAGATTCACAAATGACTATGCAAGAAAGAACTAT 132
Db 253 AATTCGTATGATACCTTTAGCAAGCAATCAACGACCATTAACAAACATGAACTAT 312
Qy 133 AAGAAATGCTAATATATGATGATTAATTAATTAATTAATTAATTAATTAATTAAT 192
Db 313 AAGATTAATGAGAAATGCTGAG-----GAGAGAAATCTGAATTA 354
Qy 193 TCTAGCCCTGAAAGCTGTTTAATGATGATGATGATGATGATGATGATGATGATGAT 252
Db 355 TTTGGAATCTCGAAGCGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 414
Qy 253 GGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 312
Db 415 GGTCAAGTATCGGGGCTTTAGGGGTTCAATTCGTCGACAGATGCTAATTTTATAGT 474
Qy 313 AGGCTAATAGTATTTATGAGGCAAGGCT-----GATCAATTTGAAAGCACTTATAGT 366
Db 475 TTGATTTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 534
Qy 367 CTGTTGTAAGAGCTTATTAAGAAAGATATGATGATGATGATGATGATGATGATGATGAT 426
Db 535 CAAGTGAATATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 594
Qy 427 GAGCTGAAGAGTTTACGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 486
Db 595 GAGCTACAGAGATTAAGAGATGCTTATGATGATGATGATGATGATGATGATGATGATGAT 654
Qy 487 GTTACAAAGATATGACA---ATCGAGGCACTAGTAAAGCATATGCAATTTGTTGAT 543

Db 655 AAAAAATGATATATACAGAGCTAGAAAGTGTGTGTGACCAATTAATTAATTAATTAAT 714
Qy 544 AACTTTTCGAAAGATATATGCAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 603
Db 715 CTGATTTTGTCTAATAATCCATCTTTGCAATATCTGACAGAGAAAGTACATTAATTA 774
Qy 604 CCAATATATGACAAAGCCGGAATTTGCAATTAATTAATTAATTAATTAATTAATTAAT 663
Db 775 TCAGTATATCAACAGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 834
Qy 664 GAGACAGAGTGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 723
Db 835 GAGCAGAGTGGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 894
Qy 724 CTGATTAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 783
Db 895 GGTACCGCCCAATCTGCAAGTTATTTGTAAGTGTATTAACCTGCTTATTAATTAAT 954
Qy 784 AATGCTCAATCTCAAGATTTGAGGCTTTAATAGTTTGTACAGATTAATTAATTAAT 843
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Qy 844 ACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 903
Db 1015 CTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1074
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Db 1075 ACAACGGCCCACTTACACGGAAAGTGTATTAATTAATTAATTAATTAATTAATTAAT 1134
Qy 964 GAAAGTGAGTAGGA 979
Db 1135 AGTGATGATTTTGT 964

RESULT 7
US-08-315-468-3

/ Sequence 3, Application US/08315468
/ Patent No. 5554534
/ GENERAL INFORMATION:
/ APPLICANT: Michaels, Tracy Ellis
/ APPLICANT: Naveira, Luis
/ TITLE OF INVENTION: Process for Controlling Scarab Beetles
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: David R. Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: FL
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/315,468
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/014,941
/ FILING DATE: 01 FEB 1993
/ APPLICATION NUMBER: 07/828,430
/ FILING DATE: 30-JAN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/808,316
/ FILING DATE: 16-DEC-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794

Best Local Similarity 51.2%; Pred. No. 1,1e-46;
Matches 714; Conservative 0; Mismatches 645; Indels 36; Gaps 6;

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Qy 230 TTTTAAAGGATTTAAGAGTGAAGCTATACCTTTGGAATTAAGGGTCCCTTGGCAA 269
Db 179 TTTAAACAGGATTTGATTTGCGGGTAAATATCTTGACCTTGGGCTTTTGGCAG 238
Qy 290 GTCAATCATTTGGAATTAATAGTGAAGTATTTTATGGGCA---GGGCGCTATC 346
Db 239 GACAAAGTATAGTCTTATATAGTTTATCTTAGTGAGCTATGGCTTAAGGGAAAAATC 298
Qy 347 CATTTGAAGCATTTAGGTTCTTGTTGAAGCATTTATTAAGAAAGATATACAGCGTG 406
Db 299 AATGGGAATCTTATAGGAACATGTAGAAAGATTTATTAACAAAATAATCAACTATG 358
Qy 407 TAAGAGAAATGCTCTTAGAGAGTAAAGGTTACAGGAATTAATAGACTATATCAA 466
Db 359 CAAGAAATTAAGCACTTACAGACTTGAAGATTAAGAGATGCCCTTAGCTCTACATG 418
Qy 467 CTAGACTGCAAGCATGCTAGTTAAACAAGATGATGACA---ATCGAGGGCACTAGTAA 523
Db 419 ATTGCTGTAAGATTTGGGTTGGAATCTATTAACACAGGGCTAGAGATGTTGTCAAG 478
Qy 524 CGCAGATGCAATTTGTTGATTAATCTTTTGAAGAAAGATATGCCAAATTCAGAGAAAG 583
Db 479 GCCAATATATCGCATTAAGATGATGTTGCTTGAAGAACTACCTTCTTTGCAAGTCTG 538
Qy 584 ACTTTGAATTTTATTTGTTACAGATATATGACACAGCCGCGAATTTGCAATTTAT 643
Db 539 GAGAGAGGTACCACTTATTAACGATATATGCTCCAAAGCTGCAAAATTTATCTTAT 598
Qy 644 TAAGAGATGCTGATTAATTTTGAAGCAAGTGGCAATTAAGGATGATGAATTCGTATA 703
Db 599 TAAGAGATGCTATTTTATTTGGAAGAAAGTGGGATTTATCATCTTCAAAATTTCAACAT 658
Qy 704 ATTATATCAGACTACAGAGCTGATTAAGAAATTAAGATCAATTTGATTAACATTTATA 763
Db 659 TTTATTAACGTCAGATGGAAGAGAGAGATTTATTCGACATTTGCTGAATGTATATA 718
Qy 764 ACCAGGTTTAAATCAATTTAATGCTCAAAATGCTCAAGTTGGGTAGCTTTAATAGT 823
Db 719 GCACAGGCTTAAATTAACCTTGAAGGGTAAATGCGGAAGTTGGGTACGATTAATCAAT 778
Qy 824 TTGATCAGATGACATTAACAGTATTAATCTCGCAATTAATTTCCAACATATGATC 883
Db 779 TCCGTAGAGACATGATTTATGCTATAGTTATAGTGCATTTTCCAAGCTATATATA 838
Qy 884 CACGTAGTATCATTAGCAGTAAACGGAATTTAGTGAAGATTTATACAGATCAG 943
Db 839 CACAAATGATTCGAATTAACAGCCCACTTCAAGAGAAATATATACAGAGCAA 898
Qy 944 TAGGTTTACTGGGGATTAAGAAAGTGAAGTGAAGCTTACCTTGATTAATCTTAATA 1003
Db 899 TTGGG---ACAGTACATCCCATCCCAAGTTTACAGTACAGACTGGTAAATTAATATG 955
Qy 1004 ATACAACCTTACGCTAGTAAAGAAATTAACGAAGAGAGCTCTTCTTAATCAACTGGC 1063
Db 956 CACCTTCTCTCTGCAATAGAGGCTGCTGTGTTGCAAAACCGCATCTACCTGATTTTC 1015
Qy 1064 TTAATGATTTTGTATATA---CAAGACTAGGTAATATGCTGATGTGAGAAATA 1120
Db 1016 TAAGAAAGTATACATTTAAGCTTATTAAGTGAAGTGAAGTACAGTCAATATGATA 1075
Qy 1121 TTTGGGAGGCAATCAATTAAGTGAAGAAATGATGTTCTGAATAATCACTTACT 1180
Db 1076 TGTGGGAGGACATTAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1135
Qy 1181 TTGGTAAACGATTCATTAATCTTATCAATTTATTTATTTGGAACCTTCTGTT 1240
Db 1136 AAGGATCTAATTAATCTTATTAATCTTGAATTAATCACTTCTGAGAGCTCT 1195
Qy 1241 TCAGTATGAGTCACTTCTGATATATTTAGAGAGAGAGAGGCTTAATTAATTA 1300

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Db 1196 ATAGACGTAGTATTCGACAGGGCTGATCTATTTTAACTCAACCTGTTAATGAGTAC 1255
Qy 1301 CTAGTCAATGAGTCTGAGAGTATTTTATATCATCAATATTAATATGATGACTG 1360
Db 1256 CTAGGTTGATTTTCAATGGAATTTGCTACACATCGATCGATCTGATTAATTC---- 1311
Qy 1361 GATCTTAAAGTACGAAGTCTGCTAATCTTCAATCCCAACTAATTAATTCAGAAATAC 1420
Db 1312 --TATATCAAGGATATGCTGAATGGACGCAATTAACAGATTCAGAAATGAATTAC 1369
Qy 1421 CAGAAAGATTAACCAAGCAAGCAAGAGAGATTTACGCTATGATTTATTTAT 1480
Db 1370 CACCTGAGCAACAGACACAGCAATTAACCAATTAATGCTAATTAATTCATATAG 1429
Qy 1481 CAATTTTATGACAGCGCAAGTATTCAGGGCGTATGTTAGTCTTTAAGCTTGGTT 1540
Db 1430 -----GACTCATTTCAACATCAATGAGAGAGATTTGATTTCTT 1471
Qy 1541 GGGCACTACAGATGATGATGATTAATGCTTGAACCAAGTAAATTAATCAATAG 1600
Db 1472 GAGCGATGCTAGTGAAGATGATGATTAATGATTAATGATTAATGATTAATGATTAAT 1531
Qy 1601 ATGAGTAAAGTT 1615
Db 1532 CATTAATAAGCTT 1546

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RESULT 9

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US-08-286-870A-3
; Sequence 3, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAYLOR, RH
; APPLICANT: TIPPERT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABRY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1946 base pairs
; TYPE: nucleic acid

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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1946
US-08-286-870A-3

Query Match 11.3%; Score 231; DB 3; Length 1946;
Best Local Similarity 51.2%; Pred. No. 1.1e-46;
Matches 714; Conservative 0; Mismatches 645; Indels 36; Gaps 6;

QY 230 TTTTAAAGGATTTAAAGAGTGAAGGACTTACTTTGAAATTTAGGGGTCCTTTGGCAA 289
DB 179 TTTCAACAGGATTTGGTATTTGCGGGTAAATTAATGTTACCTTACGGGTTCTTTTGCAG 238
QY 290 GTCAATCATTTGGAATTAATAGAGCTAATAGGATTTTATGGGCA---GGGCGTGAATC 346
DB 239 GACAACTAGCTAGCTTTTATATGTTTATCTTAGGAGCTAGTGGCTTAAGGGGAAAAATC 238
QY 347 CATTTGAAGCACTTATAGTCTTGTGAGAGCTTATTAAGAAAAGTATAGATCAAGCTG 406
DB 299 AATGGGAAATCTTTATAGAAACATGTAAGAGATTTATCAAAAAATCAACTTATG 358
QY 407 TAAAGAAAATGCTCTTAAAGAGCTAAGAGTTTACAGGAATTAAGACTATATCAAA 466
DB 359 CAAGAAATTAAGCACTTACAGACTTGAAGATTAAGAGATGCTTACCTGCTACCATG 418
QY 467 CTAGACTGCAAGAGTGGCTAGTTAACAAGATGATGACA---ATCGGAGGCACTAGTA 523
DB 419 ATTCCGTTGAAAGTTGGGTTGAAATGTAATACACAGAGGCTAGAGTGTGTCAAGA 478
QY 524 CGCAGATGCAATTTGTTGATTAATCTTTTCGAAAAGATATCCAAAATTCAGAAAAAA 583
DB 479 GCCAATATATCGCAATTAAGATTAATGTTGTTGTTGCAAAATCACTTCTTTGCAGTGCTG 538
QY 584 ACTTTGAAATTTTATTTGTTACCAATATATGCAACAGCCGCAATTTGCAATTAATTTAT 643
DB 539 GAGAGGAGGTACCAATTAATCCATATATATCCCAAGCTGCAAAATTAATCAATTTGTTAT 598
QY 644 TAAAGATGCTGATTAATTTTGGAGCAAGTGGCAATTAAGTGAATGAATTCGATTA 703
DB 599 TAAAGATGCTGATTAATTTTGGAGCAAGTGGCAATTAAGTGAATTCGATTA 658
QY 704 ATTATATCAACTACAAAGACTGATTAAGAAATTAAGATCAATTTGATTAATCAATTTAT 763
DB 659 TTTATATACGCTCAAGTCGAACGAGAGATTAATTCGACCAATTTGATTAATTA 718
QY 764 ACCAGGTTTAAATCAATTTAATCGCTCAAAATGCTCAAGTTGGGAGCTTTAATAGT 823
DB 719 GCACAGGTCTAAATTAATTTGAGGGGTAACAATGCCGAAGTTGGGTAAGTATTAATCAAT 778
QY 824 TTGTAAGATTAAGCAATTAAGATTAATTAATTCGCAATTAATTTCCAAATTAATGATC 883
DB 779 TCCGTAGAGCAATGATTTTATAGTACTAATTAATTAATTAATTAATTAATTAATTAAT 838
QY 884 CACGTAGTATCCATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAG 943
DB 839 CAATAATGATCAATTAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 898
QY 944 TAGGGTTTACTGGGGATTAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1003
DB 899 TTGGG---ACAGTACATCCGATCCCAAGTTTCAAGTGAAGTGAAGTGAAGTGAAGTGA 955
QY 1004 ATTAACAATTTTACTGATTAAGAAATTAAGCAAGAGAGCTCTTCTTAATACACTTGGC 1063
DB 956 CACCTTCGTTCTCTGCAATAGAGCTGCTGTTGTTGAAAACCGCAATTAATGATTTTC 1015
QY 1064 TTAATGTAATTTTGTATATA---CAAGACTCTAGGTAATTAATGCTGATGAGAAATA 1120
DB 1016 TAGAACAAGTAAATTTACAGCTTATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1075
QY 1121 TTTGGGAGGGCAATTAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1180

DB 1076 TGTGGGAGAGCAATTAATCAATTAATTCGAAACAATTAAGAGAAAGTTAAATATCTCAAC 1135
QY 1181 TTGTTAAACATGATTTCTATTAATCTCTATTTCAATATTTTAATTTTGGGAACTTTCTGTT 1240
DB 1136 AAGATCTACTAATTAATTTCTAATTAATTCGTGAACATTAACGTTCACTTCGAGAGCTCT 1195
QY 1241 TCAGATTAAGTCACTTCTCTGTAATTAATTAAGAGAAACAGAGCTTAATTAATTAATTA 1300
DB 1196 ATAGCAATTAATTAATTAAGAGAGCTGTAATTAATTAATTAATTAATTAATTAATTA 1255
QY 1301 CTAGTCAATTAAGAGAGCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1360
DB 1256 CTAGGTTGATTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1311
QY 1361 GATCTTAAGATTAAGAGAGCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1420
DB 1312 ---TATTAATCAAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1369
QY 1421 CAGAAAGATTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1480
DB 1370 CACCTGAACCAAG 1429
QY 1481 CAAATTTGATGACAGGAG 1540
DB 1430 -----GACTCATTTGAGCATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1471
QY 1541 GGGCAATACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1600
DB 1472 GAGCGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1531
QY 1601 ATGCACTTAAGGTT 1615
DB 1532 CATTAGTAAAGCTT 1546

RESULT 10
US-08-460-570-1
Sequence 1, Application US/08460570
Patent No. 5965797
GENERAL INFORMATION:
APPLICANT: BLENK, ROBERT G.
APPLICANT: ELY, SUSAN
APPLICANT: TAILOR, RAVINDRA H.
APPLICANT: TIPPERT, JANET M.
TITLE OF INVENTION: BACTERIAL GENES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: CUSHMAN DABRY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,570
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/520,228
FILING DATE: 09-MAY-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE NUMBER: 218875/PS.35271/US/N

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 861-3000
 TELEFAX: (202) 822-0944
 TELEX: 6714627 CUSH
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2965 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 US-08-460-570-1

Query Match 11.24; Score 229.4; DB 2; Length 2965;
 Best Local Similarity 51.14; Pred. No. 3.2e-46;
 Matches 713; Conservative 0; Mismatches 646; Indels 36; Gaps 6;

230 TTTTAAACGGGTATTAACAGGTAGAGGACTATCTTTCGAAATTTTGGGCTCCCTTTGGCAA 289
 533 TTCAAAACAGGTATGTGATTTGCGGGTAAATTAATCTGTACCTTACGGGCTCTTTTGGCAG 592
 290 GTCATCATTTGGATTAATATAGTACGCTAATAGGATTTTATGGGCA---GGGCTGATC 346
 593 GACAAGAGTACTAGCTTTATATAGTTTATCTTAGGTGAGCTATGAGCTTAAGGGGAAAAATC 652
 347 CATTTGAAAGCACTTATAGTCTTGTGAAAGAGCTTTATTAAGAAAAGTATAGATCAGCGTG 406
 653 AATGGGAATCTTTATGGAACATGATAGAGATTATTAATCAAAAAATATCAACTATG 712
 407 TAAGAGAAAATGCTCTTAGAGAGCTAGAGAGTTTACAGGAATTTATGACTATATCAA 466
 713 CAGGAATTAAGACCTTACAGACTTGAAGATTAAGAGATGCTTATAGCTGTCTACCATG 772
 467 CTAGACTGCAAGAGTGGCTAGTTAACAAGATGATGACA---ATCGGAGGGCACTAGTAA 523
 773 ATTCGCTTGAAGTGGGTTGGAATGCTATTAATACACAGGCGCTAGAGTGTGTCAAGA 832
 524 CGCAGTATGCAATTTGTGATTAATCTTTTCGAAAAGATATGCCAAATTCAGAAAAA 583
 833 GCCAATATATCGCATTAAGATTAATGATGTTGCTTCAAGAACTCTTTTGCAGTGTCTG 892
 584 ACTTTGAAATTTTATTTGTTCCAGTATATGCAAGCCGCGAAATTTGCATTTAATTTTAT 643
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 764 ACCAGGTTTAAATCAATTTAATCGCTCAAAATGCTCAAGTTGGTGAAGCTTTAATAGT 823
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 824 TTGCTACAGTATAGACATTAACAGTATTAATCTCGCAATATTAATTTCCAAATATGATC 883
 1133 TCGGTAGAGACATGATTAATAGTACTATTAATTAAGGACATTAATTTCCAAAGCTATGATA 1192
 884 CAGGTAGTATCAGTATAGCAGTAAAAAACGAATTTGACTAGGAAGTTTATACAGATCCAG 943
 1193 CACAAATGTATCCAAATTAATAACACAGCCCACTTACAGAGAAAGTATATACAGACGCAA 1252
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 1253 TTGGG---ACAGTACATCCCATCCCAAGTTTCAAGTATGAGTATTAATTAATATG 1309
 1004 ATACAACTTTATCTGCTATAGAAAATAACGCAAGACGACTCTTCTTATACACTGGC 1063
 1310 CACCTTCTTCTCTGCTATAGAGGCTGCTGTGTGAAAACCGCACTTACAGATTTTTC 1369
 1064 TTAATGTAATTTTGTATATA---CAAGACTCTAGGTAATATGTCTGATGAGAAATA 1120

1370 TAGAACAGTTACAAATTTACAGCTTATTAAGTCAATGAGACTAACCTCAGTATATGATA 1429
 1121 TTTGGGAGGCGACATCAATTAATGTAAGAAATGATGTTCTGAAATTAACCATTAAT 1180
 1430 TGTGGGAGGACATTAATCTGAAATTCGAAACAAATAGAGAAAGCTTAATATCTCAAC 1489
 1181 TTGTAATCTGATTTATTAATCTTATTAATCTTATTAATTAATTTTATTTTGGAACTTCTGTT 1240
 1490 AAGATCTACTAATTAATCTTATTAATCTTATTAATCTTATTAATTAATTAATTAATTA 1549
 1241 TCAGTATGATCACTTCTCTGATATATTTATAGAGAGACAGGCTTAATTAATTAATTA 1300
 1550 ATGAGCTGATATTTGGCGAGGCTGATATCTATTTTAACTCAACCTGTTAAATGAGTAC 1609
 1301 CTAGTATGATGAGTCTGAGGATTAATTTTAAATCATCAATTAATTAATTAATTAATTA 1360
 1610 CTAGGTTGATTTTCAATTTGAAATTTGTCACACATCCGATCGCATCTGATTAATTTTC--- 1665
 1361 GATCTTTAAGATACGAAGTCCCTGTAATCTTCATCCCAACTATTAATTAATTAATTAAT 1420
 1666 --TATTATCAGGTTATGCTGAAATTTGGACGAATTAACAGATTCAGAAAATGAATTA 1723
 1421 CAGAAAAGATTAAGCCAAAGCAAGAGAGATTTCAAGCAATTAATTAATTAATTAAT 1480
 1724 CACCTGAGCAACAGACAGCCAAATTAATGAATCTTATAGTCATTAATTAATTAATTA 1783
 1481 CAAATTTGATGACGCGCAAGTATGCTGAGGCTGATTTGTTATCTTTTAACCTTTGGT 1540
 1784 -----GATCATTTCAAGCATCAATGTAAGAAAGCATTTGATTTCTT 1825
 1541 GGCACATACAGTATGATGATGTAATATGCTTGAACAGATTAATTAATTAATTAATTA 1600
 1826 GAGCGATCTAGTGCAGATCTGACAAATTAATTAATTAATTAATTAATTAATTAATTA 1885
 1601 ATCAGTTAAAGGT 1615
 1886 CATTAAGTAAAGCTT 1900

RESULT 11
 US-08-460-570-2
 Sequence 2, Application US/08460570
 Patent No. 5965797
 GENERAL INFORMATION:
 APPLICANT: BLENK, ROBERT G.
 APPLICANT: ELY, SUSAN
 APPLICANT: TAILOR, RAVINDRA H.
 APPLICANT: TIPPERT, JANET M.
 TITLE OF INVENTION: BACTERIAL GENES
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
 STREET: 1100 New York Avenue, N.W.
 CITY: Washington
 STATE: D. C.
 COUNTRY: U.S.A.
 ZIP: 20005-3918
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/460,570
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/520,228
 FILING DATE: 09-MAY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 8910624.9
 FILING DATE: 09-MAY-1989

```

ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 218875/PS.35271/US/N
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2965 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2965
US-08-460-570-2

Query Match      11.2%; Score 229.4; DB 2; Length 2965;
Best Local Similarity 51.1%; Pred. No. 3.2e-46;
Matches 713; Conservative 0; Mismatches 646; Indels 36; Gaps 6;

QY 230 TTTTAA CGGTATTA CAGTGA GGA CTAT ACTTTC GAATTTAG GGGTCC TTG GCA 289
DB 533 TTCAA CAGTAT TGGA TTGCG GGTAA ATACTTGG TACCTTAG GGTCTT TGGCAG 592
QY 290 GTCAATCATTTGGAATTAATTAAGGCTAATAGTATTTTAATGGCA---GGGCGTCATC 346
DB 593 GACAGATGCTAATCTTTATAGTTTATCTTAGGTGAGCTATGCGCTTAAGGGGAAAAATC 652
QY 347 CATTTGAGCACTTATGTTCTTGTGAGAGCTTATTAAGAAAAGTATAGTACAGCTG 406
DB 653 AATGGGAATCTTTATGGAACATGTAAGAGATTTATTAACAAAAATTCACATTATG 712
QY 407 TAAGAGAAATGCTCTTAGAGAGCTAGAAAGTTTACAGGAATTAATGACATATATCAA 466
DB 713 CAGGAATATAAGCACTTACAGACTTGAAGATTAAGAGATGCTTAGCTGTACCATG 772
QY 467 CTAGACTGCAAGCATGGCTAGTTTAAACAAGATGACA---ATCGAGGGCACTAGTAA 523
DB 773 ATTCGCTTGAAAGTTGGGTTGAAATCGTAATAACACAAAGGCTAGGAAGTGTGCAAG 832
QY 524 CGAGATGATGAATGTTGATTAATCTTTTCGAAAAAGAAATATCCAAATTCAGAAAAAA 583
DB 833 GCCAATATATCGCATTAAGAAATGATGTTTCCTTCAAGAACTACCTCTTTGCAAGTCTG 892
QY 584 ACTTGAATTTTATTTGTTACAGATATATACAAAGCCGGAATTTGCATTTAATTTAT 643
DB 893 GAGAGAGGATACATTAATTAACCATATATGCCCAAGCTGCAAAATTTACATTTGTGCTAT 952
QY 644 TAAGAGATGCTGATTAATTTTGGAGCACAATGGCAATTAAGTGAATGAAATTCGTGATA 703
DB 953 TAAGAGATGCTGATTAATTTTGGAAAGAGTGGGATTAATCATCTTCGAAATTTCAACAT 1012
QY 704 AATATATCACTACACAAAGCACTGATTAAGAAATTAAGATTCATTTGATTAACATTTCTATA 763
DB 1013 TTTATTAACCGTCAAGTGAACGACGAGCAAGATTAATTCCTACATTTGTAAGTATA 1072
QY 764 ACCAGGTTTAAATCAATTTAATCGCTCAATGCTCAAGATTTGGGTGAGCTTAAATAGT 823
DB 1073 GCACAGGTCTAAATTAATTTAGAGGGGTACAAATGCGAAATTTGGGTGATGATATATCAAT 1132
QY 824 TTGATACAGATATGACATTAACAGTATTAAGTCTCGCAATATTTTCCAAATCAATGATC 883
DB 1133 TCCGTAGAGACATGACTTTATAGTGTACTAGATTTAAGTGCACTAATTTCCAAAGCATGATA 1192
QY 884 CAGGTAGTTCATTTAGCAGTAAABACGGAATTTGATAGGAGTTTATACAGATCAG 943
DB 1193 CACAAATGATCCAAATTAACCTACAGCCCACTTAACAGAAAGATATATACAGACGCA 1252
QY 944 TAGGTTTACTGGGTATTAAGAAAGTGAAGTAGAATTAACCTTGTGATATATCTTATA 1003

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DB 1253 TTGGG---ACAGTACATCCGATCCAAAGTTTACAAAGTACGACTTGATTAATTAATAG 1309
QY 1004 ATACAACCTTTCTGCTATAGAAAATTAACGCAAGACAGAGTCTCTTTATACCACTTGGC 1063
DB 1310 CACCTTCGTTCTCTGCAATAGAGGCTGCTGTTGTTGGAACCGGATCTACTGATTTTC 1369
QY 1064 TTAATCGTATTTTGTATATA---CAAGACTCTAGATATATGTTGATGAGAAATA 1120
DB 1370 TAGAACAACTTACAATTTACACTTATTAATGATGATGAGTAACTAGATATATGATA 1429
QY 1121 TTTGGGAGGCACTACATTAATGTAAGAAAATGAAATGATGTTCTGAATAACCCATACT 1180
DB 1430 TGTGGGAGACATTAACCTAGAAATTCGCAACATAGAGAAACGTTAAATATCTCAACAC 1489
QY 1181 TTGTTAACTGATTTCTATTAATCTCTATTCATATTTTATTTATTTGCGAACCTTTCTGTT 1240
DB 1490 AAGGATCTACTAATCTTATTAATCCGTAACTATACCTTCACTTCCAGAGAGTCT 1549
QY 1241 TCAGTATTAAGTCACTTGTCTGTATATTAATTTAGAGAAACAGAGCTAATTAATTAATTA 1300
DB 1550 ATAGGACTGAATCATTTGCGAGGCTGATCTAATTTTAACTCAACCTGTTAATGAGATAC 1609
QY 1301 CTAGTCAGTATGAGCTCGAAGATTAATTTTAATATCATCAATATAATTAATATGATCCTG 1360
DB 1610 CTAGGCTGATTTTCAATTTGAAATTCGTACACATCCGATCGCATCTGAATATTC--- 1665
QY 1361 GATCTTTAAGATACGAGTGCCTGCTAATCTTCCATCCCAATATTAATATGAGATTAAC 1420
DB 1666 --TATTTATCAAGGATATGCTGGAATTTGGGACCCATTAACAGATTCAGAAAATGATTTAC 1723
QY 1421 CAGAAAAGATTAAGCCCAACCAACGACAGAGATTTACGCCATATGATTTATTAAT 1480
DB 1724 CACCTGAACCAACAGGACAGCCAAATTAATGAATCTTATAGTATATGATTAATTCATATAG 1783
QY 1481 CAAATTTATATGACGGGCAAGTATGTCGGCGATATTTTATGCTTTTAAGCTTTGGTT 1540
DB 1784 -----GACTCATTTTCAGATCACTGATGAAAGCATTTGATATTTCTT 1825
QY 1541 GGGCACTACCAATGATGATGATTAATTCATGCTTGAACCAAGTAAATTAATCAATAG 1600
DB 1826 GAGCGCATGCTGATGAGATCTGTAATCAATTAATTAATGAGCCAAATTAATCACAAATAC 1885
QY 1601 ATGCACTTAAGGTT 1615
DB 1886 CATTAATAAAGCTT 1900

RESULT 12
US-08-286-870A-1
; Sequence 1, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELI, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPERT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABRY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/286,870A
;
; FILING DATE: 05-AUG-1994
;
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US 07/520228
;
; FILING DATE: 09-MAY-1990
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: GB 8910624.9
;
; FILING DATE: 09-MAY-1989
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: PAUL N. KOKULIS
;
; REGISTRATION NUMBER: 16,773
;
; REFERENCE/DOCKET NUMBER: 70608/220720
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (202) 861-3000
;
; TELEFAX: (202) 822-0944
;
; INFORMATION FOR SEQ ID NO: 2:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 2965 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: both
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
;
; FEATURE:
;
; NAME/KEY: CDS
;
; LOCATION: 1..2965
;
; US-08-286-870A-2
;
Query Match      11.2%; Score 229.4; DB 3; Length 2965;
Best Local Similarity 51.1%; Pred. No. 3.2e-46;
Matches 713; Conservative 0; Mismatches 646; Indels 36; Gaps 6;
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DB      533 TTCAAACAGGTATGATGATGCGGGTAAATATCTGTGATCCCTAGGGGTTCTTTTGCA 592
QY      290 GTCAATCATTTGGAAATTAATTAAGGCTAATAAGTATTTATGGCA---GGCCCTGATC 346
DB      593 GAAAGATGAGTACTTATATGATTTTATCTTAGGTGAGCTATGCGCTAAAGGGGAAAAATC 652
QY      347 CATTTAGAGCACTATAGGTTCTTTGGAAGAGCTTATAGAAAAGATATGATCAGCGT 406
DB      653 AATGGAAATCTTTATGGAACATGTAGAAAGATTTATATCAAAAAATATCAACTTATG 712
QY      407 TAGAGAAAATGCTCTTAGAGAGCTAGAGGTTTACAGGAAATTATGACTATATCATA 466
DB      713 CAAGAAATTAAGCACTTACAGACTTGAAGGATTTAGAGATGCTTACGTGTACATG 772
QY      467 CTAGACTGACAGATGGCTATGTTAAACAAGATATGACA---ATCGAGGGCACTAGTAA 523
DB      773 ATTCGCTTGAAAGTTGGGTTGGAATCTGTAATTAACAAGAGGCTAGGAAGTGTCAAG 832
QY      524 CGAGATGAGCAATTTGTAATACCTTTTGGAAAAGAAATGCAAAATTCAGAGAAAGAA 583
DB      833 GCCAATATATCGCATTAAGATTAATGATGTCTTCAGAAAACACTCTCTTTGACGTGTG 892
QY      584 ACTTGAATTTTATTTGTTACAGTATATGACAAAGCCGCAATTTGCAATTTATTTAT 643
DB      893 GAGAGAGATGACATTAATTAATCCATATATGCCCAGCTGCAATTTTACATTTGTGCTAT 952
QY      644 TAAAGATGCTGATTAATTTTGAACAAGTGCATTTAGGTGATGAAATTCGTGATA 703
DB      953 TAAAGATGCTATTTTATTTTGAAGAAAGAGGGGATTAATCATCTTCAGAAATTTCAACAT 1012
QY      704 ATTATATCGACTACAAAGACGTATTAAGAAATATTAAGTCTTTGATTAATCACTTCTATA 763
DB      1013 TTATATACCGTCAAGTCGAACGACAGAGATTAATTCCTTACACTGTGTGAAATGGTATA 1072

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DB      1133 TCCGTAGACATGACATTTAATGATCTGATATTAATGATGATGCACTTATTCAGGCTATGATA 1192
QY      884 CAGTAGATATCCATTAAGACATTAAGAAACGAAATGTAAGGAAAGTTATATACAGATCCAG 943
DB      1193 CACAAATGATATCCAAATTAAGACATACGCCAATTTACAAAGAAAGATATATACAGACGA 1252
QY      944 TAGGGTTACTGGGGTATTAAGAAAGTGAAGTGAAGCTTACCTTGGTATATCTTAATA 1003
DB      1253 TTGGG---ACAGTACATCCGCAATCCAAAGTTTTCAGAGTGAATTAATTAATG 1309
QY      1004 ATACACCTTTACTGCTATGAGAAAATTAAGCAAGACGCTCTTTATACACTTTGGC 1063
DB      1310 CACTTCGTTCTCTGCAATAGAGGCTGCTGTTGTTGAAACCCGCACTTACCTGATTTTC 1369
QY      1064 TTAATGCTATTTTGTATATA---CAAGACTCTAGTAAATATGCTGATGTAGAAATA 1120
DB      1370 TAGAACAGTTTCAATTTACAGCTTATTTAAGTGAATGAGTACACTGATATATGATA 1429
QY      1121 TTTGGGAGGGCATACATTAGTTGAAATGAAATGATGTTCTGAAATTAACCATPACT 1180
DB      1430 TGTGGGAGGACATTAATAGAAATTCGAAACATAGAGAAAGTTAAATATCTCAACAC 1489
QY      1181 TTGCTAAACGTATCTATATACCTCAATCAATATTTAATTTGGGACCTTCTGTTT 1240
DB      1490 AAGGATCTACTAATCTCTATTAATCTGTAAATTCGTAACATTAACGTTCACTTCGAGAGCT 1549
QY      1241 TCAGATATGATCACTCTGCTGATATATTTTGAAGAAACAGAGGCTAAATATTAATTA 1300
DB      1550 ATAGACTGATATCTTGGCAGGGCTGATCTATTTTAACTCAACCTGTTATGAGATAC 1609
QY      1301 CTATGATGATGAGTCTGAGAGTATTTTAAATCATCAATTAATTAATATATGTA 1360
DB      1610 CTAGGGTATATTTCTATGGAATTCGTCAACATCCGATCGCATCTGATTAATTTTC--- 1665
QY      1361 GATCTTTAAGATACGAAGTGCTGCTATATCTTCCATCCCAACTAATTAATCAAGATTTAC 1420
DB      1666 --TATATATCAGGGTATGCTGAATTTGGAACGCAATTAACAGATTAAGAAATGAAATTA 1723
QY      1421 CAGAAAGGATTAAGCCAAAGCAAGCAAGAGATTTACGCCATAGATTAATCTTATATAT 1480
DB      1724 CACCTGAAACACAGACAGCCAAATTAATGAAATCTTATATGCTATATATCTCATATAG 1783
QY      1481 CAAATTTGATSCACGCGCAAGTATGTTCAAGCGGTATTTGTTTAACTTTGGTT 1540
DB      1784 -----GACTCATTTCAAGCATTCACATGTGAAGAGCATTTGATATTTCTT 1825
QY      1541 GGGCAGATACAGATATGATCTGTAATATCTGTTGAACCAATTAATTAATCTCAAAATG 1600
DB      1826 GGAACGATCTGTGTGAGATCTGTAATTAATTAATTAATTAATTAATTAATTAATTA 1885
QY      1601 ATGAGTTAAAGTT 1615
DB      1886 CATTAATTAAGCTT 1900

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RESULT 14
US-08-448-170-7
; Sequence 7, Application US/08448170
; Patent No. 5723758
;
; GENERAL INFORMATION:
;
; APPLICANT: Payne, Jewel
;
; APPLICANT: Cummings, David A.
;
; APPLICANT: Cannon, Raymond J.C.
;
; APPLICANT: Narva, Kenneth E.
;
; APPLICANT: Steiman, Steve
;
; TITLE OF INVENTION: No. 5723758e1 Bacillus thuringiensis Isolate Denoted

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; TITLE OF INVENTION: B.c. PS158C2, Active Against Lepidopteran Pests, and Genes
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Salimanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,170
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Salimanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-448-170-7

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Query Match      10.9%; Score 223.6; DB 2; Length 3684;
Best Local Similarity 51.9%; Pred. No 9,1e-45;
Matches 655; Conservative 0; Mismatches 589; Indels 18; Gaps 6;

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; 227 CTGTTTAAAGGATTTAACAAGTGAAGGACTATCTTTCGAATTTAGGGGTCCTTTTG 286
; 164 CAGTCAAAAGGATTTAACAAGTGAAGGACTATCTTTCGAATTTAGGGGTCCTTTTG 223
; 287 CAAATCAATCTTTGGAATTAATTAAGGCTAATAGGATTTATGAGGCA---GGGCTG 343
; 224 CTGGAAATATAGCTAGTTTATATGTTTCTTGTGTGTAATATAGCCCGGGGAGAG 283
; 344 ATCCATTGAGAGCTTATAGGCTTCTTGTGAAGGCTTATAGAAAAGTATAGATCAGC 403
; 284 ATCTTGGGAATTTTCTTGAAGAGTGCAGACACTATTAACAACAAGTAACAGAA 343
; 404 GTGTAAAGAAAATGCTCTTGAAGAGCTAGAGGTTTACAGGAATATAGACTATATC 463
; 344 ATACTAGGGATTAAGGCTCTTGTCTCGATTAACAAGTTTGAAGAAATCTTTAGAGCTATC 403
; 464 AAATCTGACTGCAGAGTGGCTAGTAAACAAGATGATG---ACAATCGAGGGCACTAG 520
; 404 AACAGTCACTGGAATGCTGTAAGAAAACCGTATGATGCAAGAGAGAGTGTCTTT 463
; 521 TAACGAGTATGGAATGTTGTAATCTTTTTCGAAAAGATATGCCAAAATTCAGAGAA 580
; 464 ATACCCAAATATATAGCTTGAAGCTTGAATTTCTTAATGAGATGCGCTTTTGCAATTA 523
; 581 GAAACTTGAATTTATTTGTTACAGATATATGACAAAGCCGGAATTTGCATTTAATTT 640

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; 524 GAAACCAAGAAATTCATTAATATGATATATGCTCAAGCTGCAAAATTAACCTATATAT 583
; 641 TATTAAGAGATGCTGATTAATTTTGGAGACAGTGGCAATTAAGGATGATGAATTCGTG 700
; 584 TATTAAGAGATGCTGCTCTTTTGGTATGTAATTTGGGCTTAATCCCAAGAAATTCAC 643
; 701 ATAAATATATCAAGCTAACAAGACTGATTAAGAAATTAAGATATCATTTATTAACATCT 760
; 644 GTTATATAGAGCCCAAGTGAAGAAAACAGAGAAATTTCTGATTAATGGCAAGATGT 703
; 761 ATACCAAGGTTTAATCAATTTAATCGCTCAATGTCTCAAGTATGGGTAGCTTATATA 820
; 704 ATATACGGGTTTAATTAATTTAAGAGGCAAAATGCTGAAGTGTGTCGATATATATC 763
; 821 GATTGCTACAGATATGACATTAACATGATTAATGATCTCGCAATATTAATTCACAACTATG 880
; 764 AATTCGTAAGAGCTTAACGCTTAGAGTATTAATCTAGTGGCACTATTCACAGCTATG 823
; 881 ATCCAGTATGATATTCATTAAGCAATTAAGCAAGATTAAGCAAGTATTAACAGATC 940
; 824 ACAAGGCTGTTTATCAATTAAGCAATTAAGCAAGTATTAAGCAAGTATTAACAGATC 883
; 941 CAGTAGGCTTACTGGGATTTAGAAAGTGAAGTGAAGTACTTCCCTGGATATATCTTA 1000
; 884 CAATGGGGAACAAATGCACTTCAGAGATTTGCAAGTACGAA---TTGGTTTAATATA 940
; 1001 ATATCAACCTTACTGCTATGAGAAATTAAGCAAGAGCAAGCTCTCTTATACACTT 1060
; 941 ATGACACATGCTTTCTGCTATGAGGCTGCTGCTTTATAGGCTCCGCACTTACTGAT 1000
; 1061 GGC---TTAATCGTATTTTGTATATACAAGACTAGTAAATATGCTGATGAGAA 1117
; 1001 TTCCAGAACGCTTACATTTTCAAGGATTAATAGTGAATGAGTAAATACCAATATATGA 1060
; 1118 ATATTTGGAGGCGCATACATTAGTGAATGAAATGATGCTTGAATATACCATTA 1177
; 1061 ATTAAGTGGGAGACATGACTGAATTCGGAACAAATTAAGGGGCTATTAATGATCCTGGA 1120
; 1178 ACTTGTAAATATGATGCTATGATCTCTTATCAATATTTTATTCGGGAACCTTTCTG 1237
; 1121 CACAGCAATATCAATATCTTATTAATCTGTAACATTAACATTCACATCTCGAGACG 1180
; 1238 TTTTCAATATGATGCTGCTGCTATATATTTAGAGGAAACAGAGGCTAATATATATA 1297
; 1181 TTTATGAACAGATCATTTTGCAGGATTAATATCTTCAATCTCCTGTAATAGAG 1240
; 1298 TTAATGATGATGAGTCTCGAGATTAATTTTAATATCATCAATTAATTAATGATAC 1357
; 1241 TACCTTGGGCTAGATTTAATTTGAGAAATCCCTGAAT---TCTCTTAGAGTAGCCTTC 1297
; 1358 CTGATCTTTAAGATACGAAGTCCCTGTAATCTTCAATCCCAACTATATATTCGAAT 1417
; 1298 TCTATATATAGGATTAATCTGAGTGGGAGACAACTATATTTGA---TTCAAGAACTGAAT 1354
; 1418 TACCAGAAAGATTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1477
; 1355 TACCACCAAGAAACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1414
; 1478 TA 1479
; 1415 TA 1416

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RESULT 15
US-08-961-803-5
; Sequence 5, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve

```



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/ TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
/ TITLE OF INVENTION: B.t. PS158c2, Active Against Lepidopteran Pests, and Genes
/ NUMBER OF SEQUENCES: 10
/ ADDRESS: Jay M. Sanders
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/961,803
/ FILING DATE: 31-OCT-1997
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/069,902
/ FILING DATE: 01-JUNE-1993
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/759,247
/ FILING DATE: 13-SEPT-1991
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/448,170
/ FILING DATE: 23-MAY-1995
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sanders, Jay M.
/ REGISTRATION NUMBER: 39,355
/ REFERENCE/DOCKET NUMBER: M/S 102DCD1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 375-8100
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3684 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-961-803-5

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Query Match 10.9%; Score 223.6; DB 3; Length 3684;
Best Local Similarity 51.9%; Pred. No. 9.1e-45;
Matches 655; Conservative 0; Mismatches 589; Indels 18; Gaps 6;

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QY 227 CTTCTTTAAGCGGATTAAGAGTGAAGTAACTACTTTCGAAATTGAGGGGTCCTTTGG 286
DB 164 CACTCCAAAGGGATTAACATGCTGTGAAGAACTAGAGTGTATTAAGGGGATCCGTTG 223
QY 287 CAAGTCATCATTTGGAATATTAGTAGGCTAAATAGTATTTTATGGGCA---GGGCTG 343
DB 224 CTGAGCAAAATAGCTAGTTTATAGTTTCTGTGTGTAATTAAGCCCCGGGCGAG 283
QY 344 ATCCATTTGAAGCACTTAGGCTTCTGTGTAAGAGCTTATTAAGAAAAGTATGATCAGC 403
DB 284 ATCTTGGGAAATTTCTCTAGAACATGTGCAACAACTTATAGCAACAAGTAAAGAAA 343
QY 404 GTGTAGAGAAATGCTCTTAGAGAGCTAGAGGTTTACAGGGAATTAAGACTATATC 463
DB 344 ATACTGAGGATAGCGCTCTGCTCGATTACAGGTTTGAAGAAATTCCTTTAGAGCTATC 403
QY 464 AAACAGACTGCAAGCATGGCTGATTAAACAAGATGATG---ACAATCGAGGCGACTAG 520
DB 404 AACAGTCACCTTGAAATGGCTGAGAAAACCGTATGATGCAAGAACAGAAAGTGTCTTT 463
QY 521 TAAAGCATATGCAATTTGTTAATCTTTTCGAAAAAGAAATATGCCAAATTCAGAGAA 580

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DB 464 ATACCAATATATAGCTTAGAATCTTGATTTCTTATGCGAGTCCGCTTTGCAATTA 523
QY 581 GAAACTTTGAAATTTATTTGTTTACAGTATATGACAAAGCCGGAATTTGCAATTAATTT 640
DB 524 GAAACCAAGAAATGCTATTTATATATGATATGCTGAAAGTGAATTTTACACTTATAT 583
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DB 764 AATTCGTAGAGCTTAACGCTAGAGATTAATGATCTAGTGGCATAATCCCAAGCTATG 823
QY 881 ATCCAGATAGATATCCATATAGACATTAACGGAATTTGCTAGGGAAGTTTATACAGATC 940
DB 824 ACACGGGTATTATCCAAATGAATACCAAGTCAATTAACAAAGAAATTTATACAGATC 883
QY 941 CAGTAGGATTTTACTGCGGATTTAGAAAGTGAAGTGAAGCTTAACCTTGATATATCTTA 1000
DB 884 CATTTGGAGAACAAATGACACCTGAGATTTTGCAATGACGAA---TTGGTTAATATA 940
QY 1001 ATAAATCAACTTTACTGCTATGGAATAAAGCAAGACAGCTCTTCTTAATCAACTT 1060
DB 941 ATGACCATATGTTTCTGCAATAGAGCTGCGTTTATAGGCTCTCGCATCTTAATGAT 1000
QY 1061 GGC---TTAATGATATTTTGTATATACAGAGCTAGGTAATATGTCATGATGAGAA 1117
DB 1001 TTCCAGAACAGCTTACAAATTTTCAAGGATTTAATGATGAGATTAATCTCAATATATGA 1060
QY 1118 ATATTTGGGAGGAGCATCAATTAAGTGAATAAGAAATGATGTTCTGAATAACCATTA 1177
DB 1061 ATTACTGGGTGGGACATTAAGCTTAATCGGAAACAATAAGGGGCTCATTAAGTACCGA 1120
QY 1178 ACTTTGTAAACTGATTTCTATTAATCTCTTAATCAATTTTAATTTGCGGAACCTTTCTG 1237
DB 1121 CACACGGAATAACAATTAATCTTAATATCTGTAACATTAACAGTTCAATCTCGAGACG 1180
QY 1238 TTTTCAGATTAAGTACATTTGCTCGTATATATTTAGAGGAACAAGGCTAATATATATA 1297
DB 1181 TTTATAGAACAGATCAATTTGACAGGATTAATTAATCTTCTTAATCTCTGTAATGAG 1240
QY 1298 TTAATGCAATGATGAGTCTCGAGAGTATTTTATATCATCAATAATTAATATATGATC 1357
DB 1241 TACTTTGGGCTAGATTTAATTTGAGAAATCCCTGAT---TCTCTTAAGAGTATGCTTC 1297
QY 1358 CTGGAATCTTAAGATTAAGAAAGTGCCTGTAATTTCCATCCAACTATATTTATCAGAAT 1417
DB 1298 TCTATCTATAGGGATTAATCTGAGTGGGACACAACATATTTGA---TTCAAGAACTGAAT 1354
QY 1418 TACCAAGAAAGATTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1477
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QY 1478 TA 1479
DB 1415 TA 1416

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Search completed: December 24, 2005, 18:55:45
Job time : 401 secs


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Db 10 AATAATCAAAATGATATGAAATTTATAGATGCAACCTTCTA---CTTCTGATCCAAAT 66
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Qy 133 AAGAAATGGCTAAATATGTGTGATTCAAATATACAAATTTATGTGTATATAGACAGTAT 192
Db 127 AAGATTTATTTAAATATGTCGCGGAAATGCTATGTAATACCTCGTGCTCA----- 177
Qy 193 TCTAGCCCTGAAAGCTGTTTAAGTATACGAGATGCTGTTTAAAGGATATTAACAGTAT 252
Db 178 -----CTGAAATGACTTGTATACGCAAGATGCGATAGGCGCAATGTAATAGTA 231
Qy 253 GGGACTATACCTTTCGAATTTAGAGGGTCCCTTTGGCAAGTCAATCATTTGGAAATTAAT 312
Db 232 GGTAAATTTACTATCAGTTTAAAGGGTCCCAATTTGTTGGCCGATAGTATCTTTTACT 291
Qy 313 AGGCTAATAGTATTTTATGCGAGGGCTGA-----TCCATTTGAAAGCACTTATGTT 366
Db 292 CAATTTATTTGATATTCGTGCGCTTCAGGGGAAAGATGCAATGGGAAATTTTATGAA 351
Qy 367 CTGTGTTGAAGAGCTTATTAAGAAAAGTATGATCAGCGTGTAGAGAAAATGCTTTAGA 426
Db 352 CAGTGAAGAACTCATTTATCAAAAATATGCAAAATATGCAAGAAATAAAGGCTTTG 411
Qy 427 GAGCTGAAGGTTTACAGGGAATTTATGAGACTATATCAAACTAGACTGCAAGCATGCTA 486
Db 412 GAATTTGAAGCATTTAGTAAATATATACCAATTTATCTTAACTGCGCTTGAAGAAATG 471
Qy 487 GTTAAACAAGATATGACAAATCGAGGGCACTAGT---AACGAGTATGCAATGTTGAT 543
Db 472 GAAATATCCAAATGCTTCAGAGGCTTACAGATGCGGAAATGCAATTTGAAATCTGAT 531
Qy 544 AACTTTTGAAGAAAGATATGCCAAATTTCAAGAAAGAACTTTGAAATTTATTTGTTA 603
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Qy 604 CCAGTATATGCAACAAGCGGCAATTTGCAATTTATTTTATTAAGAGTGTGATTTATTT 663
Db 592 ACTGTATATGCAATGCGAGCCAACTTCAATTTACTGTATTTAAAGAGCGGCTCAATTT 651
Qy 664 GGAGCAAGTGGCAATTAAGTGAATGAATTCGTATATTAATATACACTACAGCTACA 723
Db 652 GGAAGAAATGGGGAATGCTCAACAACACTATTAATATACATTTATATGCTCAATGAA 711
Qy 724 CTGATTAAGAAATATTAAGATCTTGTATATACATTTCTATACAGAGGTTTAAATCA 783
Db 712 CTTACTGCAAGAAATTTCTGATCACTGTATAGTGTATGAATCTGTTTAAAGCAAA 771
Qy 784 AATCGCTCAAAATGCTCAAGATTTGGGTGAGCTTTATATAGTTTGTACAGATATGACAT 843
Db 772 AAGGCAAGAGCGCTTAACATATGAGTGTGACTATTAACCAATTCGTAAGAAATGAC 831
Qy 844 ACAGTATTAATCTCCCAATATTTATTTCCAACTATGATCCAGTATGATTCATTTAG 903
Db 832 GCGGTTTATGATTTGTGCAATTTATCCCAATTTATGACACAGCAAGTATCCCAAT 891
Qy 904 GTTAAAGGCAATTTAGCTAGGGAAGTTTATACAGATCCAGTATG 947
Db 892 ACGAAAGCAACACTTAACAGGGAATATATACAGATCCACTGG 935
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RESULT 2
US-11-108-389-11

Sequence 11, Application US/11108389
Publication No. US2005026118A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu

```
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnall
APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: US/11/108,389
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PaetSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 2010
TYPE: DNA
ORGANISM: Bacillus thuringiensis (truncated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2010)
FEATURE:
NAME/KEY: misc.feature
LOCATION: (0)...(0)
OTHER INFORMATION: 1218-1A
US-11-108-389-11
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Query Match 11.5%; Score 235.6; DB 7; Length 2010;
Best Local Similarity 56.5%; Pred. No. 7,5e-45;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

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Qy 13 AAAAAAAGAAATGAAATGTTGATGCTTTACGAATCAACTTAATATGCTAAT 72
Db 10 AATAATCAAAATGAAATATGAAATTTATAGATGCAACCTTCTA---CTTCTGATCCAAAT 66
Qy 73 TGTATTCAGAGTATCCACTAGCAAAAAGATCCAAATGACTATGCGAAAACAGAACTAT 132
Db 67 GATTCTTAACAGATACCTTTTGGCAATGAGCCCAACAAATGCGTTACAAAATATGATAT 126
Qy 133 AAGAAATGGCTAAATATGTGTGATTCAAATATACAAATTTATGTGTATATAGACAGTAT 192
Db 127 AAGATTTATTTAAATATGTCGCGGAAATGCTATGTAATACCTCGTGCTCA----- 177
Qy 193 TCTAGCCCTGAAAGCTGTTTAAGTATACGAGATGCTGTTTAAAGGATATTAACAGTAT 252
Db 178 -----CTGAAATGACTTGTATACGCAAGATGCGATAGGCGCAATGTAATAGTA 231
Qy 253 GGGACTATACCTTTCGAATTTAGAGGGTCCCTTTGGCAAGTCAATCATTTGGAAATTAAT 312
Db 232 GGTAAATTTACTATCAGTTTAAAGGGTCCCAATTTGTTGGCCGATAGTATCTTTTACT 291
Qy 313 AGGCTAATAGTATTTTATGCGAGGGCTGA-----TCCATTTGAAAGCACTTATGTT 366
Db 292 CAATTTATTTGATATTCGTGCGCTTCAGGGGAAAGATGCAATGGGAAATTTTATGAA 351
Qy 367 CTGTGTTGAAGAGCTTATTAAGAAAAGTATGATCAGCGTGTAGAGAAAATGCTTTAGA 426
Db 352 CAGTGAAGAACTCATTTATCAAAAATATGCAAAATATGCAAGAAATAAAGGCTTTG 411
Qy 427 GAGCTGAAGGTTTACAGGGAATTTATGAGACTATATCAAACTAGACTGCAAGCATGCTA 486
Db 412 GAATTTGAAGCATTTAGTAAATATATACCAATTTATCTTAACTGCGCTTGAAGAAATG 471
Qy 487 GTTAAACAAGATATGACAAATCGAGGGCACTAGT---AACGAGTATGCAATGTTGAT 543
Db 472 GAAATATCCAAATGCTTCAGAGGCTTACAGATGCGGAAATGCAATTTGAAATCTGAT 531
Qy 544 AACTTTTGAAGAAAGATATGCCAAATTTCAAGAAAGAACTTTGAAATTTATTTGTTA 603
Db 532 AGTTTATTTAAGCAATATATATGCAATCTTTTAAAGTGAACAATTTGAAGTACCATTC 591
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QY 604 CCAGTATATGCACAAAGCCGGAATTTGCAATTAATTTATTAAGAGATGCTGATTTT 663
DB 592 ACTGTATATGCATGAGGACCACTTCACTTACTGTATTAAGAGAGCGGTCAATTTT 651
QY 664 GGAGCAGTGGCAATTAAGTATGATGAATTCGTATTAATTAATTAATTAATTAATTA 723
DB 652 GGAGAAAGATGGGATGTGCAACAACACTATTAATTAATTAATTAATTAATTAATTA 711
QY 724 CTGATTAAGAAATTAAGATGATGATTAATTAATTAATTAATTAATTAATTAATTA 783
DB 712 CTGATTAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 771
QY 784 AATGCTCAATGCTCAAGATGGGTGAGCTTTAATGATGTTGTCAGATATGACATTA 843
DB 772 AAGGCAAGGCGCTTAACATAGGTTGATTAACCAATTCGTATGAAGAAATGACATG 831
QY 844 ACAGTATTAATGATTCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 903
DB 832 GCGTTTATGATGTTGTTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 891
QY 904 GTAAAAAGCAATTTGACTAGGAAATTAATTAATTAATTAATTAATTAATTAATTA 947
DB 892 ACGAAAGCAACACTAACAGGAAATTAATTAATTAATTAATTAATTAATTAATTA 935

RESULT 3
US-11-058-727-1
; Sequence 1, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnell
; APPLICANT: James F. H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058, 727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3621)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: CRY1218-1
; US-11-058-727-1

Query Match 11.54; Score 235.6; DB 7; Length 3621;
Best Local Similarity 56.54; Pred. No 9.2e-45;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

QY 13 AAAAAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 72
DB 10 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 66

QY 73 TGTATCAAGATATCCATAGCAAAAGATCAAAATGACTATGCGAAACAGCAATAT 132
DB 67 GATTCAAGATATACCTTTTGGGAATGAGCAAAATGCGTACAAAATATGATTAAT 126
QY 133 AAGAAATGCTAAATATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 192
DB 127 AAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 177
QY 193 TCTAGCCCTGAACTGCTTAATGATGATGATGATGATGATGATGATGATGATGATG 252
DB 178 -----CCTGAACTGCTTAATGATGATGATGATGATGATGATGATGATGATGATG 221
QY 253 GGGACTATATCTTCAATTTAGGGTCCCTTTGGCAATGATCAATTTGGAATTAATTA 312
DB 232 GTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 291
QY 313 AGGCTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 366
DB 292 CAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 351
QY 367 CTGTTGAAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 426
DB 352 CAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 411
QY 427 GAGCTAAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 486
DB 412 GAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 471
QY 487 GTTAACAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 543
DB 472 GAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 531
QY 544 AACTTTTGAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 603
DB 532 AGTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 591
QY 604 CCAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 663
DB 592 ACTGTATATGCATGAGGACCACTTCACTTACTGTATTAAGAGAGCGGTCAATTTT 651
QY 664 GGAGCAGTGGCAATTAAGTATGATGAATTCGTATTAATTAATTAATTAATTAATTA 723
DB 652 GGAGAAAGATGGGATGTGCAACAACACTATTAATTAATTAATTAATTAATTAATTA 711
QY 724 CTGATTAAGAAATTAAGATGATGATTAATTAATTAATTAATTAATTAATTAATTA 783
DB 712 CTGATTAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 771
QY 784 AATGCTCAATGCTCAAGATGGGTGAGCTTTAATGATGTTGTCAGATATGACATTA 843
DB 772 AAGGCAAGGCGCTTAACATAGGTTGATTAACCAATTCGTATGAAGAAATGACATG 831
QY 844 ACAGTATTAATGATTCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 903
DB 832 GCGTTTATGATGTTGTTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 891
QY 904 GTAAAAAGCAATTTGACTAGGAAATTAATTAATTAATTAATTAATTAATTAATTA 947
DB 892 ACGAAAGCAACACTAACAGGAAATTAATTAATTAATTAATTAATTAATTAATTA 935

RESULT 4
US-11-108-389-1
; Sequence 1, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen


```

QY 133 AAGAAATGCTAAATATGTGATTCAAATACAAATTTATGATATATAGCAGTAT 192
DB 857 AAGATATATTTAAAAATGTCTGCGGAAATCTGATGAATACCTGGTCA----- 907
QY 193 TCTAGCCTGAAGTCTCTTAAGTGTACGAGATCTGTTTAAACGGTATTAACAGTGA 252
DB 908 -----CCTAAGACTTGTGTAGCGGACAGATCAGCTAAGCGCAATTTGATATGTA 961
QY 253 GGGACTATCTTGAATTTAGGGGTCCTTGGCAAGTCAATCACTTGAATTAATAGT 312
DB 962 GGTAAATTAATAGGTTTAAAGGGTCCATTGTGGCCGATGATGATCTTAACT 1021
QY 313 AGGCTAATAGTATTTTATGGGCGAGGCTCA-----TCCATTTGAAGCACTTATGTT 366
DB 1022 CAATTAATGATANTCTGTGGCCCTTCAAGGGAAGAGTCAATGGGAAATTTTATGGA 1081
QY 367 CTGTGTAAGAGCTTATTAAGAAAAGTATAGATCAGCGGTAGAGAAAATGCTTTAGA 426
DB 1082 CAAGTAGAAGAACTCATTAATCAAAAAATAGCAAAATATCAAGAAATTAAGCGCTTCG 1141
QY 427 GAGCTGAAGTATTACAGGGAATATAGACTATATCAATCACTGCAAGCAATGGCTA 486
DB 1142 GAATTAAGAAATTAAGGTAATTAATTAACCAATTAATCACTGCTTGAAGAAATGGAA 1201
QY 487 GTTAACAAGATATGACAAATCGGAGGCACTAGT---AAGCAGTATGCAATTTGAT 543
DB 1202 GAAATTCAAATGTTTCAAGAGCTTACGAGATGCGGAAATGCAATTTGAATCTGGAT 1261
QY 544 AACTTTTTCGAAAAGAAATATGCCAAATTCAGAGAAAGAACTTTGAATTTTATGTTA 603
DB 1262 AGTTTATTTACGCAATATATGCGCATCTTTAGAGTGAACAAATTTTGAATGACATTCCT 1321
QY 604 CCAGTATATGCAAGAGCGGGAATTTGCAATTTTATTTATTAAGATGCTGATATTTT 663
DB 1322 ACTGTAATCAATGAGGACCAACCTTCATTTACTGTTATTAAGAGCGGTCATTTT 1381
QY 664 GAGCAAGTGGCAATAGGATGATGATGAATTCGTATTAATATATACACTACAGCAAGA 723
DB 1382 GAGAAAGATAGGGAATGATGCAACAACTATTAATTAATTAATGATGCTCAATGAAA 1441
QY 724 CTGATTAAGAAATATTAAGATCAATTTGTAATCAATTTCTAATCAAGGTTTAAATCAATTT 783
DB 1442 CTTACGCAAGAAATATCTGATCACTGTGTAAGTGTATGAATCTGTTTAGCAAAATTA 1501
QY 784 AATCGCTCAAAATGCTCAAGTTGGGTGAGCTTTAATAGTTTGTATCAAGATATGACATTA 843
DB 1502 AAGGCAAGCGGCTTAACAAATGAGTGAATTAACCAATTCGTTAGAGAAATGACACTG 1561
QY 844 ACAGTATTAATCTCGCAATTAATTTCCAACTATGATCAGATGATGATTCATTAAGA 903
DB 1562 GCGGTTTATATGTTGTTGCTATTAATTCGCAAAATTAATGACACGACGATACCAATGAA 1621
QY 904 GTAAAAACGAAATTAAGTAGGAAATTTATATACAGATCAGATAGG 947
DB 1622 ACGAAAGCAACAATAACAGGGAAGTATATACGATCACTGGG 1665

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; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIORITY FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ. ID NOS: 134
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ. ID NO 17
; LENGTH: 4874
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Genomic DNA 1218-1
US-11-108-389-17

Query Match 11.5%; Score 235.6; DB 7; Length 4874;
Best Local Similarity 56.5%; Pred. No. 1e-4;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

QY 13 AAAAAATTAATGAATATGAATGTTGATGCTTTACGAATCAACTTAATGCTAAT 72
DB 740 AATTAATCAAAATTAATGAATTAATATGATGCAACCTTTCA---CTTCTATTCAT 796
QY 73 TGTATCAAGATATCACTAGCAAAAGATCACAATGACTATGCGAAACAGAACTAT 132
DB 797 GATTCTAAGATATACCTTTTGGGAATGAGCAACAAATGCGTACAAAATATGATAT 856
QY 133 AAGAAATGCTAAATATGTGTATTAATCAATATCAATTTATGTGATATTAAGACGAT 192
DB 857 AAGATATTTTAAAAATGCTCGGGAAGATGTAAGTAATACCTGGTTCA----- 907
QY 193 TCTAGCCTGAAGTCTCTTAAGTGTACGAGATCTGTTTAAACGGTATTAACAGTGA 252
DB 908 -----CCTAAGACTTGTGTAGCGGACAGATCAGCTAAGCGCAATTTGATATGTA 961
QY 253 GGGACTATCTTGAATTTAGGGGTCCTTGGCAAGTCAATCACTTGAATTAATAGT 312
DB 962 GGTAAATTAATAGGTTTAAAGGGTCCATTGTGGCCGATGATGATCTTAACT 1021
QY 313 AGGCTAATAGTATTTTATGGGCGAGGCTCA-----TCCATTTGAAGCACTTATGTT 366
DB 1022 CAATTAATGATANTCTGTGGCCCTTCAAGGGAAGAGTCAATTTTATGGA 1081
QY 367 CTGTGTAAGAGCTTATTAAGAAAAGTATAGATCAGCGTATAGAAAAATGCTTTAGA 426
DB 1082 CAAGTAGAAGAACTCATTAATCAAAAAATAGCAAAATATGCAAGAAATTAAGCGCTTCG 1141
QY 427 GAGCTGAAGTATTACAGGGAATTAATGAGCTATTAATCAATGACTGCAAGAGCTGA 486
DB 1142 GAATTAAGAAATTAAGTATTAATTAATCAATTTATTAATCACTGCTGAAAGATGGA 1201
QY 487 GTTAACAAGATATGACAAATCGAGGCACTAGT---AAGCAATATGCAATTTGAT 543
DB 1202 GAAATTCAAATGTTTCAAGAGCTTACGAGATGTCGAAATGATTTGAATTCGAT 1261
QY 544 AACTTTTTCGAAAAGAAATATGCCAAATTCAGAGAAAGAACTTTGAATTTTATGTTA 603
DB 1262 AGTTTATTTACGCAATATATGCGCATCTTTAGAGTGAACAAATTTGAAGATTCCT 1321
QY 604 CCAGTATATGCAAGAGCGGGAATTTGCAATTTTATTTATTAAGATGCTGATATTTT 663
DB 1322 ACTGTAATGCAATGAGCAAGCAACCTTCATTTACTGTTATTAAGAGCGGTCATTTT 1381
QY 664 GAGCAAGTGGCAATTAAGTGTATGTAATTCGTATTAATTAATCAAGTCAAGGA 723
DB 1382 GAGAAAGATAGGGAATGATGCAACAACTAATTAATTAATGATGCTCAAAATGAAA 1441

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PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 2022
TYPE: DNA
ORGANISM: Bacillus thuringiensis (truncated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2022)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: 1218-2A
US-11-108-389-13

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Query Match 11.4%; Score 234; DB 7; Length 2022;

Best Local Similarity 56.4%; Pred. No. 1.8e-44; Matches 532; Conservative 0; Mismatches 385; Indels 27; Gaps 4;

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13 AAAAAATGAATGAAATGTTGATGCTTAACTCACTTAATATGCTAAT 72
10 AATATCAAAATGAAATGAAATATAGTCCGACCTTCTA---CTTCTGATCAAT 66
73 TGTATCAAGATGATCCATGCAAAAGATCCAAATGACTATGCAACGAACTAT 132
67 GATTCTAAGATACCTTTTGGCAATGAGCAAAATGCGCTACAAATATGATATAT 126
133 AAGAAATGCTAATATGATGATCAATACAAATTTATGCTATATAGCACTAT 192
127 AAGATATATTAATAATGTCGCGGAAATGCTAGTAATACCTGATTC----- 177
193 TCTAGCCCTGAGCTGCTTAAGTATGAGATCTGTTTAAAGGCTATTAACAGTGA 252
178 -----CTGAAATGCTGTTAGCGGACAAAGATGACACTAAGCGCAATGATATGTA 231
253 GGAATATATCTTGAATTTAGGGGCTCTTTGGCAATGCAATTTGAAATATAGT 312
232 GGTAAATATCTATGAGGTTTAAAGGGTCCATTTGTTGGCCGATAGATCTTATATCT 291
313 AGCTATATAGTATTTATGAGGCGAGGCTGA-----TCAATTTGAGCACTATAGTT 366
292 CAATTAATGATATCTGTCGCTTCAAGGCAAAAGATGCAATGGAGATTTTATGAA 351
367 CTGTTGAGAGCTTATTAAGAAAGTATGATCAGCGGTGTAAGAAATGCTCTAGA 426
352 CAAGTAAAGAACTCATTAATCAAAAATGACAGATATGCAAGAAATTAAGGCTTTG 411
427 GACCTAGAGGTTTACAGGAATTTATGAGACTATATCAAACTAGACTGCAAGCTGCTA 486
412 GAATTAAGAGATTAAGTAAATTAATCAATTAATTAATCTAATGCGCTTGAAGATGAAA 471
487 GTTAACAGATATGACATCGAGGCACTAGT---AACGAGTATGCAATTTGTTGAT 543
472 GAAATTCGAATGTTTCAGAGCTTACGAGATGTCGAAATGCAATTTGAAATTCCTGAT 531
544 AACTTTTGAAGAAATATGCAAAATTCAGAAAGAAATTTGAAATTTTATGTTA 603
532 AGTTTATTTAGCAATATGATCCATCTTTTGAAGTCAAAATTTTGAAGTACCTTCTT 591
604 CAGATATATGACAAAGCGGAAATTTGATTTATTTATTAAGAGATGCTGATTTAT 663
592 AAGATATATACAGGCAAGCACTTCAATTTACTGTTATTTAAAGAGCTTCAATTTT 651
664 GAGACAGATGCAATTAAGTATGATGAATTTGATATTTATATCAACTACAGGA 723
652 GGAAGAAATGGGATGCTCAACCACTAATTAATTAATTAATGATCGTCAAAATGAAA 711

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724 CTGATTAAGAAATTAAGATCATTGTATTAACATTCTATTAACAGGTTTAAATCAATT 783
712 CTATCTCAGAAATATCTGATCACTGTGTAAGGATGAAATCTGTTTAGCAAAATTA 771
784 AATGCTCAAAATGCTCAAGATTTGGGTAGCTTTAATAGTTTCTTAAGATATGACATTA 843
772 AAGGCAAGAGCGTAAACAATGGGTGACTATTAACCAATTCGTAAGAAATGACCTG 831
844 ACAGTATTAATCTCGCAATATTTATTTCAAACTATGATCCAGTATGATATTCATTA 903
832 ACGTTTAAATGATGTTGATTTATTTCCAAATTAATTAACACAGCAAGTACCAATGAA 891
904 GTAAAAAGCAATGACTAGGAAATTTATTAACAGATCCAGTAG 947
892 ACGAAAGCAACTAACAAGGAAGTATATACAGATCCAGTGG 935

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RESULT 9

US-11-058-727-3
Sequence 3, Application US/11058727
Publication No. US20050261483A1

GENERAL INFORMATION:

APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnall
APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
FILE REFERENCE: 35718/287809

CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15

PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26

PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04

PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25

NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 3633

TYPE: DNA

ORGANISM: Bacillus thuringiensis

FEATURE:

NAME/KEY: CDS (3633)

LOCATION: (1)...(3633)

FEATURE:

NAME/KEY: misc_feature

LOCATION: (0)...(0)

OTHER INFORMATION: CRY1218-2

US-11-058-727-3

Query Match 11.4%; Score 234; DB 7; Length 3633;
Best Local Similarity 56.4%; Pred. No. 2.2e-44; Matches 532; Conservative 0; Mismatches 385; Indels 27; Gaps 4;

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13 AAAAAATGAATGAAATGTTGATGCTTAACTCACTTAATATGCTAAT 72
10 AATATCAAAATGAAATGAAATATAGTCCGACCTTCTA---CTTCTGATCAAT 66
73 TGTATCAAGATGATCCATGCAAAAGATCCAAATGACTATGCAACGAACTAT 132
67 GATTCTAAGATACCTTTTGGCAATGAGCAAAATGCGCTACAAATATGATATAT 126
133 AAGAAATGCTAATATGATGATTTCAATTAACAAATTTATGCTATATAGCACTAT 192
127 AAGATATATTAATAATGTCGCGGAAATGCTAGTAATACCTGATTC----- 177

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193 TCTAGCCCTGAGAGCTGTTAAGTGTACGAGATGCTGTTTAAAGGGTATTAACAGTGT 252
178 -----CTGGAAGTACTTGTGTACCGACAGAGAGCGCTTAAGGCCCAATGTATATAGA 231
253 GGGACTATATCTTTCGAATTTAGGGGGTCCCTTGGCAAGTCAATCATTTGGAAATTAATAG 312
232 GGTAAATTAATCTAGGTTTAGGGGTCCCAATTTGTTGGCCGATAGTGAATCTTTTAACT 291
313 AGGCTAATAGATATTTTATGGGCAAGGCGCTGA-----TCCATTTGAAGCACTTATGTT 366
292 CAACCTATGATATCTGTGGCGCTTCAGGGCAAAAAGATCAATGGAGATTTTATAGAA 351
367 CTGTGTGAAGAGCTTTTAAAGAAAGATATGATCAGCGTGTAAAGAAAATGCTCTTAA 426
352 CAAGTGAAGAACTCAATTAATCAAAAATAGCAGAAATATGCAAGATATAAGCGCTTTGG 411
427 GAGCTGAAGGTTTACAGGGAATTAAGACCTATATCAACTGACCTGCAAGCATGGCTA 486
412 GAATTAAGAGATTAAGTAAATTAATACCAATTAATCTAACCTGCGCTTGAAGATGAAA 471
487 GTTAACAAGATGATGACATCGAGGGGCACTAGT---AACGAGTATGCAATTTGTTGAT 543
472 GAAATTCGAATGCTTCAAGAGCTTACGAGATGTGGAAATGCAATTTGAAATCCGAGAT 531
544 AACTTTTGGAAAAGAAATATGCCAAATTCAGAGAAAAGAACTTTGAAATTTTATGTTA 603
532 AGTTTATTAACGCAATATACATGCGATCTTTTCAGTACAAATTTTGAAGTACCATTCCT 591
604 CCAATTTATGCAACAGCCCGAATTTTGAATTTTAAATTTTAAAGATGCTGATTTATTT 663
592 ACAGTATATACAGAGCAGCAACCTTCATTTATGTTTAAAGACGCTTCAATTTT 651
664 GGAGCAGTGGCAATTAAGTGTATGATGAATTCGTATATATATATATCAACTACAGCA 723
652 GGAAGAAATGGGAGTGTCTACACACATTAATTAATATATATATGATGTCAAATGAAA 711
724 CTGATTAAGAAATTAAGATCATTTGTATTAACATTTCTATACAGAGGTTTAAATCAATT 783
712 CTTAATGCAAGATATTTCTGATCACTGTATTAAGTGTATGAAAATCTGTTTAAAGAAATTA 771
784 AATCGCTCAATGCTCAAGATTTGGGTGAGCTTTAATAGGTTTGTACAGATATGACATTA 843
772 AAAGCAGAGCGCTTAACATAGGTGATGATTAACCAATTCGTAGAGAAATGACACTG 831
844 ACAGTATGATTCGCAATATATTTCCAACTAGATCCAGTATGATTCATTTAGCA 903
832 ACGGTTTGAATTTTGTGATTAATTCGCAATTAATGACACAGCAGCACTGCAATGAA 891
904 GTTAAACCGAATTAAGTGAAGGAGTTTATACAGATCCAGTACG 947
892 ACGAAGCACAATTAACAGGGAATATATACAGATCCACTGG 935

RESULT 10
US-11-108-389-3
; Sequence 3, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McQuichen
; APPLICANT: James K. Presnall
; APPLICANT: James F. H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786

; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3633
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3633)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cyt1218-2
US-11-108-389-3

Query Match 11.4%; Score 234; DB 7; Length 3633;
Best local similarity 56.4%; Pred. No. 2,2e-44;
Matches 532; Conservative 0; Mismatches 385; Indels 27; Gaps 4;

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10 AATATCAAAAAGAAATATGAATTAATATAGATGACACTTCTA---CTTCTGATCAAT 66
73 TGTATCCAAAGATCCACTACCAAAAGATCCAAATGACTATGGGAAACGAACTAT 132
67 GATTTCAAGATACCTTTTGGAAATGACCAAAATGCGCTCAAAAATATGATTTAT 126
133 AAAGATGGCTAATATATGATTCAAATACAAATTAATTTGATATTAAGCAGTAT 192
127 AAAGATTAATTAATAATGCTCGGGAATGCAATGCAATCCGTGTTCA----- 177
193 TCTAGCCCTGAGAGCTGTTAAGTGTACAGATGCTGTTTAAAGGTTTAAAGTGT 252
178 -----CTGGAAGTACTTGTGTAGCGCAAGATGACAGTGAAGTGAATTAATAGA 231
253 GGAATATATCTTTCGAATTTAGGGGTCCCTTGGCAAGTCAATCATTTGGAATTAATAG 312
232 GGTAAATTAATCTAGGTTTAAAGGTTTCCATTTGTTGGCCGATAGTGAATCTTTAACT 291
313 AGGCTAATGATATTTTATGGCAGGGCGCTGA-----TCCATTTGAAGCACTTATGTT 366
292 CAACCTATGATATCTGTGCGCTTCAGGGCAAAAAGATGCAATGGAGATTTTATAGAA 351
367 CTGTGTGAAGAGCTTTTAAAGAAAGTATGATCAGCGTGTAAAGAAAATGCTCTTAA 426
352 CAAGTGAAGAACTCAATTAATCAAAAATAGCAGAAATATGCAAGATATAAGCGCTTTG 411
427 GAGCTGAAGGTTTACAGGGAATTAAGACCTATATCAACTGACCTGCAAGCATGGCTA 486
412 GAATTAAGAGATTAAGTAAATTAATACCAATTAATCTAACCTGCGCTTGAAGATGAAA 471
487 GTTAACAAGATGATGACATCGAGGGGCACTAGT---AACGAGTATGCAATTTGTTGAT 543
472 GAAATTCGAATGCTTCAAGAGCTTACGAGATGTGGAAATGCAATTTGAAATCCGAGAT 531
544 AACTTTTGGAAAAGAAATATGCCAAATTCAGAGAAAAGAACTTTGAAATTTTATGTTA 603
532 AGTTTATTAACGCAATATACATGCGATCTTTTCAGTGAACAAATTTTGAAGTACCATTC 591
604 CCAATTTATGCAACAGCCCGAATTTGCAATTTTAAATTTTAAAGATGCTGATTTATTT 663
592 ACAGTATATACAGAGCAGCAACCTTCATTTATGTTTAAAGACGCTTCAATTTT 651
664 GGAGCAGTGGCAATTAAGTGTATGATGAATTCGTATATATATATATGACTACAGCA 723
652 GGAAGAAATGGGAGTGTCTACACACATTAATTAATATATATATATGATGTCAAATGAAA 711
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Db 772 AAAGGACGAGCGCTTAAACAAATGGTTCGACTATTAACCAATTCGTGAGAGAAAGACACTG 831
Qy 844 ACAGTATAGATCTCCCAATATATTTCCAACTAGATGACGTAGGTATCCATTAGCA 903
Db 832 ACGGTTTAGATGTGTGATTTATTCACCAATTAATGACACGACGTCATCCCAATGGA 891
Qy 904 GTAAAAACGGAAATGACTAGGAAAGTTTATACAGATCCAGTAGG 947
Db 892 ACGAAAGCACTAACTAACAGGAAAGTATATACAGATCCACTGGG 935
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RESULT 11

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/ Sequence 18, Application US/11058727
/ Publication No. US20050261483A1
/ GENERAL INFORMATION:
/ APPLICANT: Andre R. Abad
/ APPLICANT: Ronald D. Flannagan
/ APPLICANT: Rafael Herrmann
/ APPLICANT: Theodore W. Kahn
/ APPLICANT: Albert L. Lu
/ APPLICANT: Billy Fred McCutchen
/ APPLICANT: James K. Presnall
/ APPLICANT: James F. H. Wong
/ APPLICANT: Cao-Guo Yu
/ TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
/ FILE REFERENCE: 35718/287809
/ CURRENT APPLICATION NUMBER: US/11/058,727
/ CURRENT FILING DATE: 2005-02-15
/ PRIOR APPLICATION NUMBER: 60/391,786
/ PRIOR FILING DATE: 2002-06-26
/ PRIOR APPLICATION NUMBER: 60/460,787
/ PRIOR FILING DATE: 2003-04-04
/ PRIOR APPLICATION NUMBER: 10/606,320
/ PRIOR FILING DATE: 2003-06-25
/ NUMBER OF SEQ ID NOS: 134
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 18
/ LENGTH: 6613
/ TYPE: DNA
/ ORGANISM: Bacillus thuringiensis
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (0)..(0)
/ OTHER INFORMATION: Genomic Ctry1218-2
US-11-058-727-18
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Query Match 11.4%; Score 234; DB 7; Length 6613;

Best Local Similarity 56.4%; Pred. No.2.6e-44;

Matches 532; Conservative 0; Mismatches 385; Indels 27; Gaps 4;

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Db 1320 GATTTCAACGATACCTTTTGGCAATGAGCCAAACAAATGCGCTACAAATATGATTAAT 1379
Qy 133 AAGAATGCTAAATATGTGTGATTCAAATACAAATTTATGATATTAAGACGATAT 192
Db 1380 AAAGATATATTTAAATATGTCTGCGGAATGCTAGGAATACCTGCTTCA----- 1430
Qy 193 TCTAGCCCTGAAGCTGCTTAACTGATACGAGATGCTGTTTAAAGGATTTAAAGATGTA 252
Db 1431 -----CTGAAATGACTTGTATGCGGACAAAGATGACGTAAAGCCGCAATGTATATAGTA 1484
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Qy 313 AGGCTAATAGGATTTTATTTAGGCGAGGCGCTGA-----TCCATTTAGACACTTAATGTT 366
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Db 1605 CAAGTAAAGAACTCTAATATCAAAAATAGCAAAATATGCAAGAAATTAAGAGCGCTTTCG 1664
Qy 427 GAGCTAAGAGTTTACAGGAAATTTATGAGACTATATCAAACTAGACTGCAAGCATGCTTA 486
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Qy 487 GTTAAACAGATGATGACAAATCGAGGCGACTAGT---AAGCATATGCAATTTGTTGAT 543
Db 1725 GAAATCCAAATGCTTCAAGAGCTTACGAGATGTGCGAAATCGATTTGAAATCCCTGAT 1784
Qy 544 AACTTTTGGAAAAGATATGCGCAAAATCAAGSAAAGAACTTGAATTTTATTTGTTA 603
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Qy 604 CCAGTATATGCACAAGCCGCAATTTGCAATTTTATTTAATTAAGAGATGCTGATTTT 653
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/ Sequence 18, Application US/11108389
/ Publication No. US20050261188A1
/ GENERAL INFORMATION:
/ APPLICANT: Andre R. Abad
/ APPLICANT: Ronald D. Flannagan
/ APPLICANT: Rafael Herrmann
/ APPLICANT: Theodore W. Kahn
/ APPLICANT: Albert L. Lu
/ APPLICANT: Billy Fred McCutchen
/ APPLICANT: James K. Presnall
/ APPLICANT: James F. H. Wong
/ APPLICANT: Cao-Guo Yu
/ TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
/ FILE REFERENCE: 35718/291049
/ CURRENT APPLICATION NUMBER: US/11/108,389
/ CURRENT FILING DATE: 2005-04-18
/ PRIOR APPLICATION NUMBER: 60/391,786
/ PRIOR FILING DATE: 2002-06-26
/ PRIOR APPLICATION NUMBER: 60/460,787
/ PRIOR FILING DATE: 2003-04-04
/ PRIOR APPLICATION NUMBER: 10/606,320
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QY 487 GTTAACAAGATGATGACAAATCGAGGGCACTAGT-----AACGCACTAT 531
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; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (2022)
US-11-058-727-25

Query Match      11.0%; Score 225.2; DB 7; Length 2022;
Best Local Similarity 55.9%; Pred. No. 1.8e-42;
Matches 534; Conservative 0; Mismatches 383; Indels 39; Gaps 4;

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QY 487 GTTAACAAGATGATGACAAATCGAGGGCACTAGT-----AACGCACTAT 531
D 472 GAAATTCGAATGGTTCAGAAAATGTTCCGGGCGCTTACAGATGTCGAAATTCATTT 531
QY 532 GCAATTTGTTATTAATCTTTTGAAGAAATATGCAAAATTCAGAGAAAGAACTTTGAA 591
D 532 GAAATCTGATAGTATTAATTAAGCAATATATGCAATCTTTAGAGTGAACAAATTTTGA 591
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QY 892 TATCAATTAAGAGTAAACGGAATGATGATGAGAAATTTAATCAATCAATCAATGAG 947

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	236	11.5	3504	US-10-089-678-2 Sequence 2, Appl1
2	236	11.5	3680	US-10-089-678-3 Sequence 3, Appl1
3	235.6	11.5	2003	US-10-032-717-5 Sequence 5, Appl1
4	235.6	11.5	2003	US-10-414-637-5 Sequence 5, Appl1
5	235.6	11.5	2010	US-10-032-717-15 Sequence 15, Appl1
6	235.6	11.5	2010	US-10-414-637-15 Sequence 15, Appl1
7	235.6	11.5	2010	US-10-606-320-11 Sequence 11, Appl1
8	235.6	11.5	2010	US-10-746-914-11 Sequence 11, Appl1
9	235.6	11.5	3621	US-10-032-717-1 Sequence 1, Appl1
10	235.6	11.5	3621	US-10-414-637-1 Sequence 1, Appl1
11	235.6	11.5	3621	US-10-606-320-1 Sequence 1, Appl1
12	235.6	11.5	3621	US-10-746-914-1 Sequence 1, Appl1
13	235.6	11.5	4874	US-10-032-717-27 Sequence 27, Appl1
14	235.6	11.5	4874	US-10-414-637-27 Sequence 27, Appl1
15	235.6	11.5	4874	US-10-606-320-17 Sequence 17, Appl1
16	235.6	11.5	4874	US-10-746-914-17 Sequence 17, Appl1
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19	234	11.4	2022	US-10-032-717-17 Sequence 17, Appl1
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21	234	11.4	2022	US-10-606-320-13 Sequence 13, Appl1
22	234	11.4	2022	US-10-746-914-13 Sequence 13, Appl1
23	234	11.4	2022	US-10-746-914-13 Sequence 13, Appl1

24	234	11.4	3633	US-10-032-717-3 Sequence 3, Appl1
25	234	11.4	3633	US-10-414-637-3 Sequence 3, Appl1
26	234	11.4	3633	US-10-606-320-3 Sequence 3, Appl1
27	234	11.4	3633	US-10-746-914-3 Sequence 3, Appl1
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29	234	11.4	6613	US-10-414-637-28 Sequence 28, Appl1
30	234	11.4	6613	US-10-606-320-18 Sequence 18, Appl1
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37	225.2	11.0	2022	US-10-414-637-11 Sequence 11, Appl1
38	225.2	11.0	2022	US-10-606-320-7 Sequence 7, Appl1
39	225.2	11.0	2022	US-10-606-320-25 Sequence 25, Appl1
40	225.2	11.0	2022	US-10-606-320-29 Sequence 29, Appl1
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42	225.2	11.0	2022	US-10-606-320-69 Sequence 69, Appl1
43	225.2	11.0	2022	US-10-746-914-7 Sequence 7, Appl1
44	225.2	11.0	2022	US-10-746-914-25 Sequence 25, Appl1
45	225.2	11.0	2022	US-10-746-914-29 Sequence 29, Appl1

ALIGNMENTS

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; Publication No. US20030017967A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichi
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, AN
; FILE REFERENCE: Q68821
; CURRENT APPLICATION NUMBER: US/10/089, 678
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 3504
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(3501)
; OTHER INFORMATION:
US-10-089-678-2
Query Match 11.5%; Score 236; DB 5; Length 3504;
Best Local Similarity 55.9%; Pred. No. 2.5e-43;
Matches 546; Conservative 0; Mismatches 400; Indels 30; Gaps 4;
QY 13 AAAAATPAAATGAATATGATGATGCTTTCGATCACTGATATATGCTAAT 72
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DB 67 AATTCCTGTTAGATACCTCTTTCGAAACGATCAACGACATTCATCAAAATGAACTAT 126
QY 133 AAGAATGCTAATATGCTGATTCATCAATATATGATATGATATGACAGCTAT 192
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QY 664 GAGACAGATGCGCAATTTAGTATGATGAATTCGTATATTTATATACAGTACAGGA 723
DB 649 GAGACAGATGCGGAAATTCACACAGAGAAATTTCCACTTTATGATCTCAGGTTGACA 708
QY 724 CTGATTAAGAAATATAAGATCATTTGATATAACTTTATATACAGGTTTAAATCAATTT 783
DB 709 CGTACCGCCCAATATCTCGAATTTATTTGTAAGTGTATACACTGCTTATGATTAATTA 768
QY 784 AATGCTCAAAATGCTCAAGATTTGGTGTAGCTTTAATAGTTTGTACAGATATGACATTA 843
DB 769 AAGATATGCAATCTGCAATTTGCTGAATGATCAACAAATTCGAAAGAAATGACATTA 828
QY 844 ACAGTATATGATCTCGCAATTTATTTTCCAACTATATACAGTATGATTTCCATTA 903
DB 829 CTGTATATGATTTAATGAGCTTATTTCCAACTATGACACAGTACGTATCCAAATCGAA 888
QY 904 GTAAAAACGGAATTTAGTAGGAATTTATACAGATCAGTAGGTTTATCGGGTATTA 963
DB 889 ACAACGGCCCACTTACACGGAAAGTATACAGATCAATATTTTACAGAAACA 948
QY 964 GAAAGTGAAGTAGA 979
DB 949 AGTGTGATTTTGTGA 964

RESULT 2
US-10-089-678-3
; Sequence 3, Application US/10089678
; Publication No. US20030017967A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
; FILE REFERENCE: 068821
; NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
; CURRENT APPLICATION NUMBER: US/10/089, 678
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3690

TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-089-678-3
Query Match 11.5%; Score 236; DB 5; Length 3690;
Best Local Similarity 55.9%; Pred. No. 2.6e-43;
Matches 546; Conservative 0; Mismatches 400; Indels 30; Gaps 4;
QY 13 AAAAAATTAATGAATATGAAAATGTTGATGCTTTAAGAAATCACTTAATATGCTAAT 72
DB 196 AATATCAAAATGAATATGAAAATTTAGATGCTTATCATCTA---CTTCTGATCCGAT 252
QY 73 TGTATCAAGATATGCACTACCAAAAGATCCCAAAATGATCTATGGGAAACAGCACTAT 132
DB 253 AATTCGTATGATACCTTTAGCAACGATCAACACACACATTTACAAAACATGAATCTAT 312
QY 133 AAGAAATGCTAAATATGATGATCAAAATATCAATTTATGATATTAAGACAGTAT 192
DB 313 AAGATATATCTGAAATGCTGAG-----GGAGAAATCTGAAATTA 354
QY 193 TCTAGCCCTGAAGCTGCTTTAAGTGTACAGATGCTGTTTAAACGGTATTAACAGTGA 252
DB 355 TTTGAAATCCGAGACGTTTATATGATCATGATGATCAAGGTTCAAACTGGAATGGCATTTG 414
QY 253 GGGACTATACCTTTCGAATTTAGGGGTCCTTTGGCAAGTCAATCATTTGGAATTAATAGT 312
DB 415 GGTCAAGTATCGGGGCTTTAGGGGTTCCATTTGCTGACAGATACGATGCTGTTTATAGT 474
QY 313 AGGCTAATAGATATTTATGAGGAGGGGCT-----GATCATTGGAAGCACTTATAGT 366
DB 475 TTCAATGTCGGTCAATTTATGCGCATCAAGTACCGTATGATGTGGAATGATATGAAA 534
QY 367 CTGTGTAAGAGCTTTAATTAAGAAATATATGATCAGCGTGTAAAGAAATGCTTTAGA 426
DB 535 CAAGTGAAGATCTAATGATCAAAAATTAACAGATTTCTGTAAGAAACAGGGCTTGA 594
QY 427 GAGCTAAGAGTTTACAGGAAATTTATGAGATCTATCAAACTATGATGCAAGATGCTA 486
DB 595 GAGCTAAGAGATTTAGAGATGCTTGAAGATATCAAGAAATCACTTTAAGAAATGGCTG 654
QY 487 GTTAAACAGATATGACAC---ATCGAGGGCACTAGTAAAGCAATGATGTTGAT 543
DB 655 GAAATTCGTATATGATCAAGAGCTAGAAAGTGTGTGTGACCAATATATAGCTTTAGAG 714
QY 544 AACTTTTGGAAAAAGATATGCCAAATTCAGAAAGAAACTTTGAAATTTTATTTGTA 603
DB 715 CTGTATTTTGTGCTAAATTTCCATCTTTGCAATATCTGACAGAAATGACATTTATTA 774
QY 604 CCAGTATATGACAGAGCCCGAAATTTGCAATTTTATTTAAGAGATGCTGATTTATTT 663
DB 775 TCAGTATATGCAACAGAGCGAAATTTTACATTTGCTATTTTACGAGATGCTTCATTTT 834
QY 664 GAGACAGATGCGCAATTTAGTGTATGATGAATTCGTATATTTATATACAGACTAACAAGA 723
DB 835 GAGACAGATGCGGAAATTCACACAGAGAAATTTCCACTTTTATATGCTGACAGTACA 894
QY 724 CTGATTAAGAAATATTAAGATCATTTGATATAACTTTATACCAAGGTTTAAATCAATTT 783
DB 895 CGTACCGCCCAATATCTCGAATTTATTTGTAAGTGTATTAACACTGCTTAGATTAATTA 954
QY 784 AATGCTCAAAATGCTCAAGATTTGGTGTAGCTTTAATAGTTTGTACAGATATGACATTA 843
DB 955 AAGGTACCAATGCTCAAGATTTGGTGTAGATATTCACCAATTTCCGAAGAGAAATGACATTA 1014
QY 844 ACAGTATGATGTCGAATTTATTTTCCAACTATGATCAGTAGTATGATTCATTAGCA 903
DB 1015 CTGTATTTAATTTATGATGCTTATTTCCAACTATGACACAGCTTATGATTCAAATGAA 1074
QY 904 GTAAAAACGGAATTTAGTAGGAATTTATACAGATCAGTAGGTTTATCGGGTATTA 963
DB 1075 ACAACGGCCCACTTACACGGAAAGTATACAGATCAATATGATTTTAAACAGAAACA 1134
QY 964 GAAAGTGAAGTAGA 979

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Db      1135 AGTGGTGAATTTGTGA 1150
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RESULT 3
US-10-032-717-5
/ Sequence 5, Application US/10032717
/ Publication No. US20020151709A1
/ GENERAL INFORMATION:
/ APPLICANT: Andre R. Abad
/ APPLICANT: Nicholas B. Duck
/ APPLICANT: Ronald D. Flannagan
/ APPLICANT: Theodore W. Kahn
/ APPLICANT: Xiang Feng
/ APPLICANT: Lynn E. Sims
/ TITLE OF INVENTION: Gene Encoding No. US20020151709A1e1 Proteins With
/ TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
/ FILE REFERENCE: 35718/237005
/ CURRENT FILING DATE: 2001-10-23
/ PRIOR APPLICATION NUMBER: 60/242,838
/ PRIOR FILING DATE: 2000-10-24
/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5
/ LENGTH: 2003
/ TYPE: DNA
/ ORGANISM: Bacillus thuringiensis (truncated)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(2001)
/ NAME/KEY: misc_feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: 1218-1
US-10-032-717-5

Query Match      11.5%; Score 235.6; DB 5; Length 2003;
Best Local Similarity 56.5%; Pred. No. 2,4e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

Qy      13 AAAAAATGAATGATGAAATGTTGATGCTTTAGCAATCACTTAATATGCTAAT 72
      |||
Db      10 AATATCAATGAATGAAATGAAATGATGACACCTTCTA---CTTCTGATCCAAAT 66
      |||
Qy      73 TGTATCAAGATGATCACTAGCAAGAAAGATCACAATGACTATGCGAAACAGAACTAT 132
      |||
Db      67 GATTTCAACGATACCTTTTGGCAATGACCAACAATCGCTACAAATATGATAT 126
      |||
Qy      133 AAGAAATGCTAATATGATGATTCATATACCAATTTATGATATATAGCACTAT 192
      |||
Db      127 AAGATTTATTTAAATATGCTGGGGAAATGCTAGTGAATACCTGGTTCA----- 177
      |||
Qy      193 TCTAGCCCTGAGCTGCTTTAAGTATGAGATGCTGTTTAAACGGTATTAACAGTGA 232
      |||
Db      178 -----CTGAAATGACTGTTAGCGGCAAGATGCAAGCTAAGCCGCAATTTGATATGTA 231
      |||
Qy      253 GGGACTATCTTTCAATTTAGGGGTCCTTTGGCAAGTCAATTTGGAATTAATAGT 312
      |||
Db      232 GGTAAATTTACTATCAGTTTAGGGGTCCTTGTGGGCCAATGATGATCTTTTACT 291
      |||
Qy      313 AGGCTAATAGTATTTTATGGGCAAGGCTGA-----TCCATTTGAAAGCACTTAATGTT 366
      |||
Db      292 CAAGTTATGATTTCTGTGGCTTCAAGGGGAAAGATGCAATGGGAAATTTTATGGA 351
      |||
Qy      367 CTGTGTAAGAGCTTATTAAGAAAGTATAGATCAGCGTGTAAAGAAAATGCTCTTGA 426
      |||
Db      352 CAAGTAAAGAACTATTAATCAAAAATAGCAGAAATATCAAGATTAAGCGCTTCG 411
      |||
Qy      427 GAGCTGAAGGTTTACAGGAATTTATGAGCTATTAATCAACTGATCGAAGCATGGCTA 486
      |||
Db      412 GAATTTGAAGGATTTAGTATTAATTAATCAATTAATTAATGCTGCTTGAAGAAATGGAA 471
      |||
Qy      487 GTTAAAGAAATGATGCAATCGAAGGCACTAGT--AAGCAATATGCAATTTGTTAT 543
      |||
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Db      472 GAAATTCAAATGTTTCAAGAGCTTACGAGATGTGCAATGATTTGAATCCGGAT 531
      |||
Qy      544 AACTTTTTCGAAAAGATATATGCAAAATTCAGAAAAGAACTTTGAATTTTATGTTA 603
      |||
Db      532 AGTTTATTTACGAATATATATGCAATCTTTTATGATGCAAAATTTGAAGATCACTTCCT 591
      |||
Qy      604 CAGATATATGACAAAGCCGGAATTTGCAATTTAATTTTATTAAGAGATGCTGATTTATTT 663
      |||
Db      592 ACTGATATATCAATGGAAGCCCAACTTCAATTTACTGTTATTTAAAGACGGCTCAATTTT 651
      |||
Qy      664 GAGACAGTGGCAATTAAGTATGATGAAATTCGTGATTAATTAATCAACTACAAAGA 723
      |||
Db      652 GGAAGAAATGAGGATGTTCAACAACCTACTAATTAATCAATTAATGATGTCGCAATGAAA 711
      |||
Qy      724 CTGATTAAGAAATTAAGATCAATTTGATTAATCAATTTCAACAGGCTTTAAATCAATTT 783
      |||
Db      712 CTTACTGCAAAATTTCTGATCTGTTGATTAATGATGATTAATCTGTTTATGCAAAATTA 771
      |||
Qy      784 AATGCTCAATGCTCAAGATTTGGTGAAGCTTTAATAGTTTGTACAGATATGACATTA 843
      |||
Db      772 AAGGACAGAGCCCTAAACAAATGGTTGACTATTAACCAATTCGTAGAGAAATGACACTG 831
      |||
Qy      844 ACGATATGATCTCCGAATTTATTTCCAAACTATGATCCAGTATGATTCATTAAGCA 903
      |||
Db      832 GCGGTTTATGATGTTGTCATTAATCCCAATTAATGACACAGCAGTACCAATGAAA 891
      |||
Qy      904 GTAAAAACGGAATGACTAGGAAAGTTTATATAGATCCAGTATAG 947
      |||
Db      892 ACGAAGCACACTAACAGGAAATTAATATACATCACTGAG 935
      |||

RESULT 4
US-10-414-637-5
/ Sequence 5, Application US/10414637
/ Publication No. US20030177528A1
/ GENERAL INFORMATION:
/ APPLICANT: Andre R. Abad
/ APPLICANT: Nicholas B. Duck
/ APPLICANT: Xiang Feng
/ APPLICANT: Ronald D. Flannagan
/ APPLICANT: Theodore W. Kahn
/ APPLICANT: Lynn E. Sims
/ TITLE OF INVENTION: Gene Encoding No. US20030177528A1e1 Proteins With
/ TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
/ FILE REFERENCE: 35718/237005
/ CURRENT FILING DATE: 2003-04-16
/ PRIOR APPLICATION NUMBER: US/10/032,717
/ PRIOR FILING DATE: 2001-10-23
/ PRIOR APPLICATION NUMBER: 60/242,838
/ PRIOR FILING DATE: 2000-10-24
/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5
/ LENGTH: 2003
/ TYPE: DNA
/ ORGANISM: Bacillus thuringiensis (truncated)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(2001)
/ NAME/KEY: misc_feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: 1218-1
US-10-414-637-5

Query Match      11.5%; Score 235.6; DB 6; Length 2003;
Best Local Similarity 56.5%; Pred. No. 2,4e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

Qy      13 AAAAAATGAATGATGAAATGTTGATGCTTTAAGCAATCACTTAATATGCTAAT 72
      |||
```

```

Db      10 AATAATCAAAATGAATGAAATTATAGATGCAACCTTCTA---CTTCTGATCCAAAT 66
Qy      73 TGTATTCAGAGTATCCATGACGAAAAAGATCCAAATGACTATGCGAAACAGAACTAT 132
Db      67 GATTCTAACGATACCTTTTGGGAATGAGCCAAACAAATGCGTACAAAATATAGANTAT 126
Qy      133 AAAAATGCGTAAATATGTTGATTCAAATPACAAATTTATGTTGATATTAAGACGAT 192
Db      127 AAAGATATTTAAAAATGTCGCGGAAATGCTAGTAATACCTGGTCA----- 177
Qy      193 TCTAGCCCTGAGCTGCTTAAAGTATGAGATGCGCTTTTAAACGGTATTAACAGTGA 252
Db      178 -----CTGAAGACTTGTATGAGGACAAAGATGCAAGCTAAGCCGCAATGATATAGTA 231
Qy      253 GGGACTATACCTTTCGAATTTAGGGGCTCCCTTGGCAAGTCAATCATTTGGAATTAATAGT 312
Db      232 GGTAAATTAATTAATCAGGTTTAAAGGGCTCCATTTGTTGGCCGATAGAGATCTTTATCT 291
Qy      313 AGGCTAATAGGATTTTATGAGGCGAGGGCTGA-----TCCATTTGAAGCACTTATGCTT 366
Db      292 CAATTAATGATATTTCTGCGCTTCAGGGGAAAGATCAATGCGAAATTTTATGGA 351
Qy      367 CTGTGTAAGAGCTTATTAAGAAAAAGTATAGATCAGGCTGTAAGAAAAATGCTCTTAGA 426
Db      352 CAAGTAAAGAACTCATTAATCAAAAAATAGCAGAAATATGCAAGAAATTAAGCGCTTTCG 411
Qy      427 GAGCTAGAGGTTTACAGGAAATATGAGACTATATCAACTAGACTGCAAGCATGGCTA 486
Db      412 GAATTAAGAGATTAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 471
Qy      487 GTTAAACAAGATATGACAAATCGAGGGCACTAGT---AAGCAGATATGCAATTTGAT 543
Db      472 GAAATATCAATGCTTCAAGAGCTTACAGATATGCAATGCAATTTGAAATCTGAGAT 531
Qy      544 AACTTTTTCGAAAAGATATGCCAAATTCAGAGAAAGAACTTGAATTTATTTGTA 603
Db      532 AGTTTATTTACGCAATTAATATGCAATCTTTAGAGTGACAAATTTGAAATGCAATTCCTT 591
Qy      604 CCAATATATGCAACAAGCGGGAATTTGCAATTTATTTTAAAGATGCTGATATTTT 653
Db      592 ACTGTAATATGCAATGCAAGCCCACTTCAATTTACTGTTATTAAGACGCGTCAATTTT 651
Qy      664 GAGACACATGCGCAATTAAGTATGATGAAATTCGTATTAATTAATTAATTAATTAATTA 723
Db      652 GGAAGAAATGCGGATGCTCAACAACACTATTAAATTAATTAATTAATTAATTAATTA 711
Qy      724 CTGATTAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 783
Db      712 CTTAATGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 771
Qy      784 AATCGCTCAATGCTCAAGATTTGGGTGAGCTTTAATAGTTTGGTACAGATATGACATTA 843
Db      772 AAAGGACGAGCGCTTAACATAGGTTGATTAATTAATTAATTAATTAATTAATTAATTA 831
Qy      844 ACAGATTAATGATCTCGCAATTAATTTCAAACTATGATCCAGTATGATTAATTAATTA 903
Db      832 GCGGTTTAAATGTTGTTGATTAATTTCCAAATTAATTAATTAATTAATTAATTAATTA 891
Qy      904 GTTAAAAAGGAATTAAGTGAAGAAATTTATTAACAGATCAAGTATG 947
Db      892 ACGAAGACAACTAACAGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 935

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RESULT 5
US-10-032-717-15

; Sequence 15, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn

```

; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1A
; US-10-032-717-15

```

Query Match 11.5%; Score 235.6; DB 5; Length 2010;
Best Local Similarity 56.5%; Pred. No. 2.4e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

```

Qy      13 AAAAAATCAAAATGAATATGAAATGTTGATGCTTTACGATCAACTATATATGCTAAT 72
Db      10 AATAATCAAAATGAATGAAATTATAGATGCAACCTTCTA---CTTCTGATCCAAAT 66
Qy      73 TGTATTCAGAGTATCCATGACGAAAAAGATCCAAATGACTATGCGAAACAGAACTAT 132
Db      67 GATTCTAACGATACCTTTTGGGAATGAGCCAAACAAATGCGTACAAAATATAGANTAT 126
Qy      133 AAAAATGCGTAAATATGTTGATTCAAATPACAAATTTATGTTGATATTAAGACGAT 192
Db      127 AAAGATATTTAAAAATGTCGCGGAAATGCTAGTAATACCTGGTCA----- 177
Qy      193 TCTAGCCCTGAGCTGCTTAAAGTATGAGATGCGCTTTTAAACGGTATTAACAGTGA 252
Db      178 -----CTGAAGACTTGTATGAGGACAAAGATGCAAGCTAAGCCGCAATGATATAGTA 231
Qy      253 GGGACTATACCTTTCGAATTTAGGGGCTCCCTTGGCAAGTCAATCATTTGGAATTAATAGT 312
Db      232 GGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 711
Qy      313 AGGCTAATAGGATTTTATGAGGCGAGGGCTGA-----TCCATTTGAAGCACTTATGCTT 366
Db      292 CAATTAATGATATTTCTGCGCTTCAGGGGAAAGATCAATGCGAAATTTTATGGA 351
Qy      367 CTGTGTAAGAGCTTATTAAGAAAAAGTATAGATCAGGCTGTAAGAAAAATGCTCTTAGA 426
Db      352 CAAGTAAAGAACTCATTAATCAAAAAATAGCAGAAATATGCAAGAAATTAAGCGCTTTCG 411
Qy      427 GAGCTAGAGGTTTACAGGAAATATGAGACTATATCAACTAGACTGCAAGCATGGCTA 486
Db      412 GAATTAAGAGATTAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 471
Qy      487 GTTAAACAAGATATGACAAATCGAGGGCACTAGT---AAGCAGATATGCAATTTGAT 543
Db      472 GAAATATCAATGCTTCAAGAGCTTACAGATATGCAATGCAATTTGAAATCTGAGAT 531
Qy      544 AACTTTTTCGAAAAGATATGCCAAATTTCAAGAAAGAACTTGAATTTATTTGTTA 603
Db      532 AGTTTATTTACGCAATTAATATGCAATCTTTAGAGTGACAAATTTGAAATGCAATTCCTT 591
Qy      604 CCAATATATGCAACAAGCGGGAATTTGCAATTTATTTTAAAGATGCTGATATTTT 653
Db      592 ACTGTAATATGCAATGCAAGCCCACTTCAATTTACTGTTATTAAGACGCGTCAATTTT 651
Qy      664 GAGACACATGCGCAATTAAGTATGATGAAATTCGTATTAATTAATTAATTAATTAATTA 723
Db      652 GGAAGAAATGCGGATGCTCAACAACACTATTAAATTAATTAATTAATTAATTAATTA 711

```

```

Qy 724 CTGATTAGAGATATTAAGATTCATTGTATTAACATTCATTAACAGGGTTTAAATCAATT 783
Db 712 CTTACTGCAAAATATTTCTGATCTGCTGTAAGGATGATGAATCGTTTAAAGAAATTA 771
Qy 784 AATGCTCAAAATGCTCAAGATGGGTGAGCTTTAATAGTTTGGTACAGATATGACATTA 843
Db 772 AAAGGCACGAGCGCTAAACAATGGGTGACTATTAACCAATTCCTGAGAAATGACACTG 831
Qy 844 ACAGTATTATATCTCGCAATATTAATTCGAAACATGATCAGCTAGTATTCATTCGCA 903
Db 832 GCGGTTTAAATGTTGTTGCAATTAATCCCAATTAATACACAGCAGCAATCCCAATGAA 891
Qy 904 GTAAAAACGGAATTTGACTAGGAGTTTATACAGATCCAGTAGG 947
Db 892 ACGAAGACACACTAACAGGGAAGTATATACAGATCCACTGGG 935

```

RESULT 6

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US-10-414-637-15
; Sequence 15, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/414,637
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1A
; US-10-414-637-15

```

```

Query Match 11.5%; Score 235.6; DB 6; Length 2010;
Best Local Similarity 56.5%; Pred. No. 2,4e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

```

```

Qy 13 AAAAATTAATGATATGAAATGTTGGATGCTTTACGAATCACTTAATATGCTAAT 72
Db 10 AATATATCAAAATGATATGAAATTAATGATGCGACACTTCTA---CTTCTGATCCAAAT 66
Qy 73 TGTATTCAGATGATCCACTAGCAAAAGATCCCAAAATGATGCTATGCGAAACGAACTAT 132
Db 67 GATTCTACAGATATCCCTTTTGGCAATGACGCAACAATGCTGCTACAAATATGATTAAT 126
Qy 133 AAAGATGCTTAATATGATGATTCAAATACAAATTTATGTTGATATAGCACTAT 192
Db 127 AAGATATATTTAAATATGCTGCGGAAATGCTAGTAATACCTGTTCA-----177
Qy 193 TCTAGCCCTGAAGCTGTTTAAGTATCGAGATGCTGTTTAAAGGATATTAACAGTGA 252
Db 178 -----CTGTAAATCTTTGTTAGCGGCAAGATGCACTAAGCCGCAATGATATATAGTA 231

```

```

Qy 253 GGAATATACCTTTCGAATTTTAAAGGGTCCCTTTGGCAAGTCAATCTTTGGAATTAATAGT 312
Db 232 GGTAAATTAATCAAGGTTTAAAGGGTCCATTTGTTGGCCGATAGATGATCTTTAATACT 291
Qy 313 AGGCTAATAGATATTTTATGCGGAGGGCTGA-----TCCATTTGAAGCACTTAATGTT 366
Db 292 CAATTAATGATATTTCTGTGCGCTTTCAGGGGAAAGATCAATGGGAAATTTTATGAA 351
Qy 367 CTGTTGGAAGGCTTATTAAGAAAGATATAGATCAGCGTGTAAAGAAATGCTCTAGA 426
Db 352 CAAGTAAAGAACTCATTAATCAAAAATGCAAGATATGCAAGAAATTAAGGCTTTG 411
Qy 427 GAGCTAAGAGTTTACAGGGAATTAAGACATATATCAAACTAGCTCAAGCATGCTA 486
Db 412 GAATTAAGAGATTTAGTATTAATTAATTAATCAATTAATCTAATCTGCTGTAAGATGGAA 471
Qy 487 GTTAACAAAGATATGACATTCGAGGGCACTGT--AACGAGTATGCAATTTGTTAT 543
Db 472 GAAATCCAAATGTTTCMAAGCCTTAAGATGTCGAAATGATTTGAAATCCTGGAT 531
Qy 544 AACTTTTGAAAAGATATATGCCAAATTCAGAGAAAGAACTTTGAAATTTTATTTGTTA 603
Db 532 AGTTTATTTAGCAATATATGCAATCTTTTAGGTGACAAATTTGAAATGCAATTCCTT 591
Qy 604 CCAGTATATGCAAGCGCGCAATTTGCAATTAATTTATTAAGATGCTGATTAATTTT 663
Db 592 ACTGATATGCAATGAGGAGCAACCTTCATTTACTGTTATTAAGACGCGTCAATTTT 651
Qy 664 GAGACAGTGGCAATTTAGTATGATGAATTCGATATTTATTAATCACTACATCAAGGA 723
Db 652 GGAAGAAATGAGGATGTCACACACTATTAATTAATTAATTAATGATGCTCAATGAAA 711
Qy 724 CTGATTAGAGATATTAAGATTCATTGTATTAACATTCATTAACAGGGTTTAAATCAATT 783
Db 712 CTTACTGCAAAATATTTCTGATCTGCTGTAAGGATGATGAATCGTTTAAAGAAATTA 771
Qy 784 AATGCTCAAAATGCTCAAGATGGGTGAGCTTTAATAGTTTGGTACAGATATGACATTA 843
Db 772 AAAGGCACGAGCGCTAAACAATGGGTGACTATTAACCAATTCCTGAGAAATGACACTG 831
Qy 844 ACAGTATTATATCTCGCAATATTAATTCGAAACATGATCAGCTAGTATTCATTCGCA 903
Db 832 GCGGTTTAAATGTTGTTGCAATTAATCCCAATTAATACACAGCAGCAATCCCAATGAA 891
Qy 904 GTAAAAACGGAATTTGACTAGGAGTTTATACAGATCCAGTAGG 947
Db 892 ACGAAGACACACTAACAGGGAAGTATATACAGATCCACTGGG 935

```

RESULT 7

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US-10-606-320-11
; Sequence 11, Application US/10606320
; Publication No. US20040091505A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: Cao-Quo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/263948
; CURRENT APPLICATION NUMBER: US/10/606,320
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 134

```


QY 427 GAGCTAGAGGTTACAGGGAATTATGAGCTATCAACTAGACTGCAGAGTGGCTA 486
DB 412 GAATTGAAAGATAGATATATATATCAATTTATCTAATCTGCGCTGAGAAATGGAA 471
QY 487 GTTACAGAGATGATGACAACTGGAGGCACTAGT--AACGAGATATGCAATGTTGAT 543
DB 472 GAAATATCCAAATGGTTCAGAGAGCTTACAGAGATGTCGAAATGCAATTTGAAATCTGGAT 531
QY 544 AACTTTTTCGAAAGATATGCGAAATTCAGAGAAAGAACTTTGAAATTTTATGTTA 603
DB 532 AGTTTATTTTACGCAATATATGCTCATCTTTTATGAGTACAAATTTTGAAGTACCATTCCTT 591
QY 604 CCAGTATATGACAGAGCCGGAATTTGCAATTTTATTTATTAAGATGCTGATTTATTT 663
DB 592 ACTGTATATGCAATGTCAGAGCAACCTTCATTTACTGTATTTAAGAGACGGTCAATTTT 651
QY 664 GGAGCACTGTCGAATTAAGTATGATGAAATTCGTATATATATATATATATATATATATAT 723
DB 652 GGAGAAATATGGGATGTCACAACTATATATATATATATATATATATATATATATATATAT 711
QY 724 CTGATTAAGAAAT 783
DB 712 CTTACTGCAAGAAATATCTGATCTATGTAAGTGTATGAAACCTGTTTATGCAAAATTA 771
QY 784 AATCGCTCAATGCTCAAGATGAGTGGTATGATGATGATGATGATGATGATGATGATGATGAT 843
DB 772 AAGGACAGAGGCTTAAACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 831
QY 844 ACAGTATATGATCTGCAAT 903
DB 832 GGGGTTTATGATGTTGTTGATATATCCAAATTTATATGACACGCACTGATCCCAATGGA 891
QY 904 GTTAAACGGAATTAAGTATGAGGAAATTTATATATATATATATATATATATATATATAT 947
DB 892 ACGAAAGCACTAACTAAAGGAAATATATATATATATATATATATATATATATATATATAT 935

RESULT 9

US-10-032-717-1
; Sequence 1, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032, 717
; PRIOR FILING DATE: 2001-10-23
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3621)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cyt1218-1
US-10-032-717-1

Query Match 11.5%; Score 235.6; DB 5; Length 3621;
Best Local Similarity 56.5%; Pred. No. 3.1e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

QY 13 AAAAAATGAATATGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 72
DB 10 AATATATCAAT 66
QY 73 TGTATTCAGAGAT 132
DB 67 GATTTTACAGAT 126
QY 133 AAGATATGCTAAT 192
DB 127 AAGAT 177
QY 193 TTAGGCTGAGAGCTCTTAAAT 252
DB 178 -----CTGAGTACTTGTATGAGGACAAAGATGAGTCAAGGCGCAATATATATATAT 231
QY 253 GGAGTATATCTTGAATTTAGGGGTCCTTGGCAATGATCATCTTTGGAATATATATATAT 312
DB 232 GGTAAATTTAT 291
QY 313 AGGCTAAT 366
DB 292 CAAT 351
QY 367 CTGTTGAAGAGCTTAT 426
DB 352 CAAGTAAAGAACTAT 411
QY 427 GAGTAAAGAGTTTACAGGAAAT 486
DB 412 GAATTAAGAGAT 471
QY 487 GTTAAACAGAT 543
DB 472 GAAATTCGAATGCTTCAAGAGCTTACAGAGATGTCGAAATGATTTGAAATCTGGAT 531
QY 544 AACTTTTTCGAAAGAT 603
DB 532 AGTTTATTTACGCAAT 591
QY 604 CCAGTATATGACAGAGCCGGAATTTGCAATTTTATTTATATATATATATATATATATAT 663
DB 592 ACTGTATATGCAATGTCAGAGCAACCTTCATTTACTGTATTTAAGAGACGGTCAATTTT 651
QY 664 GGAGCACTGTCGAATTAAGTATGATGAAATTCGTATATATATATATATATATATATATAT 723
DB 652 GGAGAAATATGGGATGTCACAACTATATATATATATATATATATATATATATATATATAT 711
QY 724 CTGATTAAGAAAT 783
DB 712 CTTACTGCAAGAAATATCTGATCTATGTAAGTGTATGAAACCTGTTTATGCAAAATTA 771
QY 784 AATCGCTCAATGCTCAAGATGAGTGGTATGATGATGATGATGATGATGATGATGATGATGAT 843
DB 772 AAGGACAGAGGCTTAAACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 831
QY 844 ACAGTATATGATCTGCAAT 903
DB 832 GGGGTTTATGATGTTTGTGATATATCCAAATTTATATATATATATATATATATATATAT 891
QY 904 GTTAAACGGAATTAAGTATGAGGAAATTTATATATATATATATATATATATATATATAT 947
DB 892 ACGAAAGCACTAACTAAAGGAAATATATATATATATATATATATATATATATATATATAT 935

RESULT 10

US-10-414-637-1
; Sequence 1, Application US/10414637
; Publication No. US20030177528A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck


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QY 133 AAGAAATGGCTAAATATGTGATTCATAATACAAATTTATGATATAGACAGCTAT 192
Db 127 AAGATATATTTAAAAATGTGCGGGAATGCTAGTAATACCTGGTCA----- 177
QY 193 TCTAGCCCTGAAGCTCTTTAAGTGTACGAGATCTGTTTAAACGGATTTAACAAGTGA 252
Db 178 -----CCTGAAGACTGTGTAGCGGACAAAGATCAGCTAAGCGCGCAATGATATAGTA 231
QY 253 GGGACTATCTTGTGAATTTAGGGGTCCTTTGCGAGTCAATCATTTGGAATTAATAGT 312
Db 232 GGTAAATTAATCAATAGGTTTAGGGGTCCTTGTGGCGGATGAGTCTTTAACT 291
QY 313 AGGCTAATAGGATTTTATGCGGAGGCTCTGA-----TCCATTTGAAGCACTTATGTT 366
Db 292 CAATTAATGATATCTGTGCGCTTCAAGGGGAAAGATGCAATGGGAAATTTTATAGAA 351
QY 367 CTGTGTAAGAGCTTATTAAAGAAAGTATAGATCAGCGTGAAGAAATGCTCTTGA 426
Db 352 CAAGTAAAGAACTCAATTAATCAAAAATAGCAAAATATGCAAGAAATTAAGCGCTTTCG 411
QY 427 GAGCTAAGGTTTACAGGGAATATGAGACTATATCAATCACTGCAAGCAATGGCTA 486
Db 412 GAATTAAGAAATGATAGGTAAATTAATACCAATTAATCTAATCTGCTTGAAGATGGAA 471
QY 487 GTTAAACAAGATGATGACAAATCGGAGGCACTAGT---AAGCAGTATGCAATTTGAT 543
Db 472 GAAATTCAAATATGTTCAAGAGCTTACAGATGTGGAAATGCAATTTGAAATCTGAT 531
QY 544 AACTTTTTCGAAAAGAAATATGCCAAAATTCAGAGAAAGAACTTTGAAATTTTATGTTA 603
Db 532 AGTTATTTTACGCAATATATATGCCATCTTTAGAGTGAACAATTTGAAGTACATTCCTT 591
QY 604 CCAATATATGCAAAAGCCGCGGAAATTTGCAATTTAATTTTAAAGATGCTGATATTTT 663
Db 592 ACTGTAATGCAATGCAAGCCCAACCTTCACTTTACGTTATTTAAAGAGCGGTCAATTTT 651
QY 664 GGAGCAAGTGGCAATTAGGTGATGATGAATTCGTGATTAATTAATCACTCAAGGA 723
Db 652 GGAGAAAGATGGGATGTGCAACAACATTAATTAATTAATTAATTAATTAATTAATTA 711
QY 724 CTGATTAAGAAATATTAAGATTCATTTGATTAACATTTCTAATCAAGGTTTAAATCAATTT 783
Db 712 CTTACTGCAAAATTTCTGATCACTGTGTAAGTGTATGAATCTGTTAGCAAAATTTA 771
QY 784 AATCGCTCAAAATGTCAAGATGGGTGAGCTTTAATAGGTTTGTACAAGATAGCACTTA 843
Db 772 AAAGGCAAGCGCTTAAACAATGGGTGACATTAATCAATTCCTGAGAAATGACACTG 831
QY 844 ACAGTATTAGATCTCGCAATTAATTTCAAACTATGATCAGTAGTATTCATTTGCA 903
Db 832 GCGGTTTAAATGTTGTTGCTATTAATTCCAAAATTAATACACGCACTGATCCCAATGAA 891
QY 904 GTAAAAACGGAATTTAGTAGGAAATTTATATACAGATCCAGTAGG 947
Db 892 ACGAAAGCAACAATTAACAAGGAAATATATACGATCCTGCG 995

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RESULT 12
US-10-746-914-1
; Sequence 1, Application US/10746914
; Publication No. US20040210963A1
; GENERAL INFORMATION:
; APPLICANT: Albert L. Lu
; TITLE OF INVENTION: Gene Encoding Proteins With Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/268350
; CURRENT APPLICATION NUMBER: US/10/746,914
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04

```

```

; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3621)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cry12Ib-1
US-10-746-914-1

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```

Query Match 11.5%; Score 235.6; DB 8; Length 3621;
Best Local Similarity 56.5%; Pred. No. 3.1e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

```

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QY 13 AAAAATTAATAATGAAATGTTGATGCTTTACGATCAATCTAATATGCTAAT 72
Db 10 AATTAATCAAAATGAAATATGAAATTAATGATGCAACCTTCTA---CTTGTATCAAT 66
QY 73 TGTATCAAGTATCCATCAGCAAAAAGATCCCAAAATGACTATGCGAAACAGAACTAT 132
Db 67 GATTTACAGATATACCTTTTGGAAATGAGCCCAACAAATGCGTACAAAATATGATTA 126
QY 133 AAGAAATGGCTAAATATGTGTGATTCAAATATACAAATTTATGATATAGCAAGTAT 192
Db 127 AAGATATATTTAAATATATGTCGCGGAAATGTATGAAATACCTGGTCA----- 177
QY 193 TCTAGCCCTGAAGCTCTTTAAGTGTACGAGATCTGTTTAAACGGTATTAACAGTGA 252
Db 178 -----CCTGAAGACTGTGTAGCGGACAAAGATCAGCTAAGCGCGCAATTTGATATAGTA 231
QY 253 GGGACTAATCTTGAATTTAGGGGTCCTTTGCGAGTCAATCATTTGGAATTAATAGT 312
Db 232 GGTAAATTAATCAATAGGTTTAGGGGTCCTTGTGGCGGATGAGTCTTTAACT 291
QY 313 AGGCTAATAGGATTTTATGCGGAGGCTCTGA-----TCCATTTGAAGCACTTATGTT 366
Db 292 CAATTAATGATATCTGTGCGCTTCAAGGGGAAAGATGCAATTTGAAATTTTATAGAA 351
QY 367 CTGTGTAAGAGCTTATTAAAGAAAGTATGATCAGGCTTAAAGAAATGCTCTTGA 426
Db 352 CAAGTAAAGAACTCAATTAATCAAAAATAGCAAAATATGCAAGAAATTAAGCGCTTTCG 411
QY 427 GAGCTAAGGTTTACAGGGAATTTATGAGACTATTAATCAATCACTGCAAGCATGGCTA 486
Db 412 GAATTAAGAAATTTAGGTAAATTAATTAATCAATTAATTAATTAATTAATTAATTA 471
QY 487 GTTAAACAAGATGATGACAAATCGGAGGCACTAGT---AAGCAGTATGCAATTTGAT 543
Db 472 GAAATTCAAATATGTTCAAGAGCTTACAGATGTGGAAATGCAATTTGAAATCTGAT 531
QY 544 AACTTTTTCGAAAAGAAATATGCCAAAATTCAGAGAAAGAACTTTGAAATTTTATGTTA 603
Db 532 AGTTATTTTACGCAATATATATGCCATCTTTAGAGTGAACAATTTGAAATGATTCCTT 591
QY 604 CCAATATATGCAAAAGCCGCGGAAATTTGCAATTTAATTTTAAAGATGCTGATATTTT 663
Db 592 ACTGTAATGCAATGCAAGCCCAACCTTCACTTTACGTTATTTAAAGAGCGGTCAATTTT 651
QY 664 GGAGCAAGTGGCAATTAGGTGATGAAATTCGTGATTAATTAATTAATTAATTAATTA 723
Db 652 GGAGAAAGATGGGATGTGCAACAACATTAATTAATTAATTAATTAATTAATTAATTA 711
QY 724 CTGATTAAGAAATTAAGATTCATTTGATTAACATTTCTAATCAAGGTTTAAATCAATTT 783
Db 712 CTTACTGCAAAATTTCTGATCACTGTGTAAGTGTATGAAGATGCTGTTTAAAGAAATTTA 771

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QY 784 AATCGCTCAAACTCTCAAGATTGGGTGAGCTTTAATAGAGTTTCGTACAGATATGACATTA 843
DB 772 AAAGGACGCGCCCTAAACAAATGGGTGACATTAACCAATTCCTGTAGAGAAATGACACTG 831
QY 844 ACGATTATGATCTCGCAATATATTTCCAAACTATGATCCAGTGGTATCCATTAGCA 903
DB 832 GCGGTTTATGATGTGTGTCATTAATTCCAAATTAAGACACAGCAGTACCAGAAATGGA 891
QY 904 GTAAAAACGGAATTGACTAGGGAAGTTTATACAGATCCAGTACG 947
DB 892 ACGAAAGCACACTAACAGGAAGTATATACAGATCCACTGGG 935

RESULT 13
US-11-021-115-5
; Sequence 5, Application US/11021115
; Publication No. US20050166284A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Andre
; APPLICANT: Flannagan, Ronald D.
; APPLICANT: Hermann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Bill F.
; APPLICANT: Presnall, James K.
; APPLICANT: Rice, Janet A.
; APPLICANT: Wong, James F.
; APPLICANT: Yu, Cao-Guo
; TITLE OF INVENTION: Plant Activation of Insect Toxin
; FILE REFERENCE: 035718/285836
; CURRENT APPLICATION NUMBER: US/11/021,115
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 60/532,185
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; US-11-021-115-5

Query Match 11.5%; Score 235.6; DB 10; Length 3621;
Best Local Similarity 56.5%; Pred. No. 3,1e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

QY 13 AAAAATAAAATGAATGAAATGTTGATCTTTCAGATCAACTTAATATGTCTAAT 72
DB 10 AATATCAAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 66
QY 73 TGTATCCAAAGTATCCAAAGTATCCAAAGTATCCAAAGTATCCAAAGTATCCAAAGTAT 132
DB 67 GATTTCAGAGATACCTTTTGGCAATGAGCCAAACAAATCGCTACAAATATGATTTAT 126
QY 133 AAAGATGGCTAATATGTGTGATCAAAATACAAATTTATGTGTATATAGACATAT 192
DB 127 AAAGATTTATTTAAATATGCTGGGAAAGTCAAGTAAATCCCTGTTCA----- 177
QY 193 TCTAGCCCTGAGCTGCTTAAAGTATGATGCTGTTTAAAGGATTTAAAGGATTAAGTAT 252
DB 178 -----CTGAAATGATCTTGTAGCGACAAAGATGCTAAAGCCGCAATTTGATATAGTA 231
QY 253 GGGACTATATCTTTCGAATTTAGGGGCTCCCTTGGCAAGTCAATCATTTGGAATTAATAGT 312
DB 232 GGTAAATTAATCAAGGTTTAAAGGGGCTCCATTTGTTGGCCGATGATGATCTTTATACT 291
QY 313 AGGCTAATAGATTTATTTATGGGCAAGGCTCTGA-----TCAATTTGAAGACTTAATAGT 366
DB 292 CAATTAATGATATTTCTGTGGCTTCAAGGGGAAAGATCAATTTGGAATTTATAGTA 351
QY 367 CTGTGTGAAGAGCTTTTAAAGAAAGTATGATCAGCGGTAAAGAAATTTGCTTTAGA 426
DB 352 CAAGTAAAGAACTCATTTATCAAAAAATAGCAAGATATGCAAGAAATTAAGCGCTTTG 411

QY 427 GAGCTTGAAGGTTTACAGGAAATTTATGACATTAATCAAACTAGATGCAAGATGGCTA 486
DB 412 GAATTAAGAAAGATTTAGTAAATATTAATCAATTAATATCTAATCTGCGCTTGAAGAAATGGAA 471
QY 487 GTTAAACAAAGATGATGCAATGAGAGGCACTAGT---AAGCAATGCAATTTGTGAT 543
DB 472 GAAATTCGAATGTTTCAAGAGCTTACAGAGATGTCGAATTTGAAATCTCGAT 531
QY 544 AACTTTTGAAGAAATATGCAAAATTTCAAGAAAGAACTTTGAAATTTTATTTGTTA 603
DB 532 AGTTATTTAAGCAATATATATGATCTTTTAAAGTACAAATTTTGAAGTACATTCCTT 591
QY 604 CCAATATATGACAAAGCCCGCAATTTGCAATTTTATTTTAAAGATCTGATTTATTTT 663
DB 592 ACTGATATGACAAATGACCAACTTCAATTTTAAAGATCTGATTTTAAAGATCTGATTTT 651
QY 664 GGAGCAGTGGCAATTTAGTATGATGAAATTTGATATTTATTTATGACACTACAAAG 723
DB 652 GGAAGAAATGGGATGTCACAACTACTATTTATTAATCTATTTATGATGTCAAATGAA 711
QY 724 CTGATTAGAAATATTAAGATCATTTGATATTAATCAATTTTAAACCAAGGTTTAAATCAATTT 783
DB 712 CTTACTGCAAGATATTTCTGATCAGTGTGTAAGTGTATGAAATCTGTTTAAAGAAATTA 771
QY 784 AATCGCTCAAAATGCTCAAAATTTGGGTGAGCTTTTAAAGTTCGTACAGATATGACATTA 843
DB 772 AAAGCACAAGGCTTAAACAAATGAGTTGACTATTAACAAATTCGTGAGAAATGACACTG 831
QY 844 AAGATATGATCTGCAATATTTATTTCCAACTATGATCCAGTATGATCCATTTAGCA 903
DB 832 GCGGTTTATGATGTTTGTTCATTAATTCCAAATTAAGACACAGCAGTACCAGAAATGGA 891
QY 904 GTAAAAACGGAATTGACTAGGGAAGTTTATACAGATCCAGTACG 947
DB 892 ACGAAAGCACACTAACAGGAAGTATATACAGATCCACTGGG 935

RESULT 14
US-10-032-717-27
; Sequence 27, Application US/10032717
; Publication No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins with
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 4874
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Genomic DNA 1218-1
; US-10-032-717-27

Query Match 11.5%; Score 235.6; DB 5; Length 4874;
Best Local Similarity 56.5%; Pred. No. 3,6e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

QY 13 AAAAATAAAATGAATGAAATGTTGATGCTTTACGAATCAACTTAATATGCTAAT 72

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Db      740 AATATCAAAATGAAATATATAGATGCGACACTTCTA---CTTGTATCCAAAT 796
Qy      73 TGTATCAAGATATCCACTAGCAAAAGATCCAAATGACTATGCGAAACAGAACTAT 132
Db      797 GATTCTACAGATACCTTTTGGCAATGACCAACAAATGCGTACAAAATATGATAT 856
Qy      133 AAGAAATGCTAAATATGTGTGATTCAAATACAAATTTATGTTATATAGACGAT 192
Db      857 AAGATATATTTAAATAGTCTGGCGGAAATGCTAGTAATACCTGGTTCA----- 907
Qy      193 TCTAGCCCTGAGAGTCTTTAAGTATGAGATGCTGTTTAAAGGATATTAACAGTGA 252
Db      908 -----CTGAAAGACTTGTATGAGCAAGATGCACTAAGCGCGCAATGATATGTA 961
Qy      253 GGGACTATATCTTCAATTTAAGGGGCTCTTTGGCAAGTCAATCTTTGAAATATAGT 312
Db      962 GGTAAATTAATCTACAGGTTTAAAGGGGCTCCATTTGTTGGCGCATGAGTCTTTATCT 1021
Qy      313 AGGCTAATAGTATTTTATGCGGAGGCGCTGA-----TCCATTTGAAGCACTTATGTT 366
Db      1022 CACTTATTAATGATTTCTGTGGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGAA 1081
Qy      367 CTGTGTGAAGAGCTTATTAAGAAAGATATGATCAGCGTTAAGAGAAATGCTTTAGA 426
Db      1082 CAAGTAAAGAACTCATTAATCAAAAATAGCAGAAATATGCAAGATTAAGCGCTTTCG 1141
Qy      427 GACTAGAAAGGTTTACAGGGAATTAATGAGACTATATCAATAGACTGCAAGCATGCTA 486
Db      1142 GAATTAAGAAAGATTAAGGTAATTAATTAATCAATTAATCTAATGCGCTTGAAGATGGAA 1201
Qy      487 GTTAACAAAGATATGCAATCGAGGCGACTAGT---AAGCAGATATGCAATTTGTTAT 543
Db      1202 GAAATTCCAATATGTTCAAGAGCTTACAGATGTGGAAATGATTTGAATTCCTGAT 1261
Qy      544 AACTTTTGAAGAAATATGCGCAAAATTCAGAGAAAGAACTTTGAAATTTTATGTTA 603
Db      1262 AGTTTATTTAGCAATATATGCGCATCTTTAGAGTGAACAATTTTGAATGACATTCCT 1321
Qy      604 CCAATATATGCAACAGCGCGGAATTTGCAATTTATTTTATTAAGATGTGATTTATTT 663
Db      1322 ACTGTATATGCAATGCGAGCAACCTTCATTTACTGTTATTAAGGCGGCTCAATTTT 1381
Qy      664 GGAGCAGTGGCAATATAGGTGATGATGATGATGATGATGATGATGATGATGATGATG 723
Db      1382 GGAGAAAGATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1441
Qy      724 CTGATTAAGAAATATTAAGATTCATTTGTAACAATTCATTAACAAGGTTTAAATCA 783
Db      1442 CTTACTGCAAGATATTTCTGATCACTGTGTAAGGTGATGAACCTGGTTAGCAAAATTA 1501
Qy      784 AATCGCTCAATGCTCAAGATTTGGGTGAGCTTTAATAGTTTGGTACAGATATGACATTA 843
Db      1502 AAGGCGACGAGCGCTTAACAATGGGTGACTATTAACAATTCGTAAGAAATGACCTG 1561
Qy      844 ACAGATATTAATCTCGCAATATTTTCAAACTATGATCCAGTAGATTTTCACTTATGCA 903
Db      1562 GCGGTTTAAATGATGTTGTGATTTATTCCAAAATTAATACACAGCAGTACCCAAATGAA 1621
Qy      904 GTTAAAAACGGAATTAAGTAAAGGATTTATTAAGATTCAGTAAAG 947
Db      1622 ACAGAAAGCAACAATTAACAAGGAAAGTATTAACAGATCCACTGGG 1665

```

RESULT 15
US-10-414-637-27

/ Sequence 27, Application US/10414637
/ Publication No. US2003017528A1

/ GENERAL INFORMATION:

/ APPLICANT: Andre R. Abad

/ APPLICANT: Nicholas B. Duck

/ APPLICANT: Xiang Feng

/ APPLICANT: Ronald D. Flanagan

/ APPLICANT: Theodore W. Kahn

```

/ APPLICANT: Lynn E. Sims
/ TITLE OF INVENTION: Gene Encoding No. US2003017528A1 Proteins with
/ TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
/ FILE REFERENCE: 35718/237005
/ CURRENT APPLICATION NUMBER: US/10/414,637
/ PRIOR FILING DATE: 2003-04-16
/ PRIOR APPLICATION NUMBER: US/10/032,717
/ PRIOR FILING DATE: 2001-10-23
/ PRIOR APPLICATION NUMBER: 60/242,838
/ PRIOR FILING DATE: 2000-10-24
/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: FASTSeq for Windows Version 4.0
/ SEQ ID NO 27
/ LENGTH: 4874
/ TYPE: DNA
/ ORGANISM: Bacillus thuringiensis
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Genomic DNA 1218-1
US-10-414-637-27

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Query Match 11.5%; Score 235.6; DB 6; Length 4874;
Best Local Similarity 56.5%; Pred. No. 3,6e-43;
Matches 533; Conservative 0; Mismatches 384; Indels 27; Gaps 4;

```

Qy      13 AAAAAATAAATGAATATGAAATGTTGATGCTTTGCAATCAACTTAATATGCTTAAT 72
Db      740 AATATCAAAATGAAATATATAGATGCGACACTTCTA---CTTGTATCCAAAT 796
Qy      73 TGTATCAAGATATCCACTAGCAAAAGATCCAAATGACTATGCGAAACAGAACTAT 132
Db      797 GATTCTACAGATACCTTTTGGCAATGACCAACAAATGCGTACAAAATATGATAT 856
Qy      133 AAGAAATGCTAAATATGTGTGATTCAAATACAAATTTATGTTATATAGACGAT 192
Db      857 AAGATATATTTAAATAGTCTGGCGGAAATGCTAGTAATACCTGGTTCA----- 907
Qy      193 TCTAGCCCTGAGAGTCTTTAAGTATGAGATGCTGTTTAAAGGATATTAACAGTGA 252
Db      908 -----CTGAAAGACTTGTATGAGCAAGATGCACTAAGCGCGCAATGATATGTA 961
Qy      253 GGGACTATATCTTCAATTTAAGGGGCTCTTTGGCAAGTCAATCTTTGAAATATAGT 312
Db      962 GGTAAATTAATCTACAGGTTTAAAGGGGCTCCATTTGTTGGCGCATGAGTCTTTATCT 1021
Qy      313 AGGCTAATAGTATTTTATGCGGAGGCGCTGA-----TCCATTTGAAGCACTTATGTT 366
Db      1022 CACTTATTAATGATTTCTGTGGCTTCAGGGGAAAGAGTCAATGCGAAATTTTATGAA 1081
Qy      367 CTGTGTGAAGAGTTTAATGAAGAAATGATGATCAGCGGTGAAGAAATGCTTTAGA 426
Db      1082 CAAGTAAAGAACTCATTAATCAAAAATGCAAGATATGCAAGAAATTAAGCGCTTTCG 1141
Qy      427 GACTAGAAAGGTTTACAGGGAATTAATGAGACTATTAACAATGACTGCAAGCATGCTA 486
Db      1142 GAATTAAGAAAGATTAAGTATATTAATTAACAATTAATTAATTAATTAAGGAGATGGA 1201
Qy      487 GTTAAACAGATATGACCAATCGAGGCGACTAGT---AAGCAGATATGCAATTTGTTAT 543
Db      1202 GAAATTCCAATATGTTCAAGAGCTTACAGATGTCGAAATGCAATTTGAAATTCCTGAT 1261
Qy      544 AACTTTTGAAGAAATATGCGCAAAATTCAGAGAAAGAACTTTGAAATTTTATGTTA 603
Db      1262 AGTTTATTTAGCAATATATGCGCATCTTTAGAGTGAACAATTTGAAATGACATTCCT 1321
Qy      604 CCAATATATGCAACAGCGGAATTTGCAATTTATTTTATTAAGATGTGATTTATTT 663
Db      1322 ACTGTATATGCAATGCGAGCAACCTTCATTTACTGTTATTAAGGCGGCTCAATTTT 1381
Qy      664 GGAGCAGTGGCAATATAGGTGATGATGATGATGATGATGATGATGATGATGATGATG 723
Db      1382 GGAGAAAGATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1441

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Qy 724 CTGATTAGAGAAATATAAAGATCATGTATATACATTCTATATACCGAGGTTTAAATCAATTT 783
Db 1442 CTTACTGCAGAAATATCTGATCACTGTATAGTGATGAAACTGGTTTAGCAAAATTA 1501
Qy 784 AATCGCTCAAAATGCTCAAGATTGGGTGAGCTTTAATAGTTTGTACAGATATGACATTA 843
Db 1502 AAAGGCAACGACGCTTAAACAATGGGTGACTATATACCAATTCGTAGAGAAATGACACTG 1561
Qy 844 ACAGTATTAGATCTCGCAATATTTCCAACTATGATCCAGTAGTATCCATTAGCA 903
Db 1562 GCGGTTTATAGATGTTGTGCAITATTCCTCAATTTATATGACACGACGTACCCAAATGAA 1621
Qy 904 GTAAAAACGAAATGACTAGGAAAGTTTATACAGATCCAGTAGG 947
Db 1622 ACGAAAGCACACTAACAAGGAAAGTATATACAGATCCACTGGG 1665

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